

7b 155

14may03 11:19:38 User:208669 Session D2288.1

\$0.28 0.081 DialUnits File1

\$0.28 Estimated cost File1

\$0.28 Estimated cost this search

\$0.28 Estimated total session cost 0.081 DialUnits

File 155:MEDLINE(R) 1966-2003/May W1

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*File 155: Medline has been reloaded and accession numbers have changed. Please see HELP NEWS 155.

Set Items Description

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7 ds

Set Items Description

S1 19809 VIRUS AND (RECEPTOR OR RECEPTORS)

S2 930316 DT=REVIEW?

S3 2087 S1 AND S2

S4 11103 S1/T1

S5 702 S4 AND S3

S6 142 SEQUENCE? AND S5

S7 25362 CAR OR HCAR OR MCAR OR COXSACKIE OR ADENOVIRUS

S8 65 S3 AND S7

S9 0 VIRAL ADJ RECEPTOR?

S10 1384 VIRAL (W) RECEPTOR?

S11 160 S2 AND S10

S12 35 S10/T1

S13 294214 MUTATION OR MUTANT

S14 593482 RECEPTOR OR RECEPTORS

S15 9325 S13 (3N)S14

S16 463 S1 AND S15

S17 24 S2 AND S16

S18 4860 S13 (N)S14

S19 232 S18 AND S1

?ts67/13

6/7/13

DIALOG(R)File 155:MEDLINE(R)

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11640582 99074492 PMID: 9852300

CD46 (membrane cofactor protein of complement, measles virus receptor); structural and functional divergence among species (review).

Seya T, Nomura M, Murakami Y, Begun N A, Matsumoto M, Nagasawa S Department of Immunology, Osaka Medical Center for Cancer and Cardiovascular Diseases, Higashinari-ku, Osaka 537, Japan.

International journal of molecular medicine (GREECE) May 1998, 1 (5) p809-16, ISSN 1107-3756 Journal Code: 9810955

Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Human CD46 was identified as a complement regulator and was later shown to be a measles virus receptor. The ubiquitous distribution profile of CD46 accounted for systemic measles infection and general protection of host tissue/organs from autologous complement. A similar ubiquitous distribution was observed for swine and simian CD46 homologues based upon subsequent cDNA cloning and Northern analysis, reinforcing the roles of CD46. In contrast, recent cDNA cloning and distribution analyses of murine and guinea-pig CD46 revealed the predominant expression of these rodent CD46 homologues in the testis, especially in mature testicular germ cells. These results do not support the established functions of human CD46 but support the hypothesis that CD46 on sperm serves as a fertilization-related adhesion molecule toward eggs. Here, we review the structure, function and distribution of human CD46 and discuss the possible differences between human CD46 and its homologues recently cloned from a variety of non-human primates and other animals. (72 Refs.)

Record Date Created: 19990224

Record Date Completed: 19990224

?ts87/2 20 26 47 53 54

8/7/2

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.

14742747 22514653 PMID: 12627395

Structural evidence for common functions and ancestry of the reovirus and adenovirus attachment proteins.

Stehle Thilo; Dermody Terence S
Laboratory of Developmental Immunology and Renal Unit, Massachusetts

General Hospital, Harvard Medical School, Boston, MA 02114, USA.
tstehle@partners.org

Reviews in medical virology (England) Mar-Apr 2003, 13 (2) p123-32,
ISSN 1052-9276 Journal Code: 9112448

Contract/Grant No.: AI38296; AI; NIAID; AI45716; AI; NIAID

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The crystal structure of the reovirus attachment protein, sigma1, reveals a fibre-like structure that is remarkably similar to that of the adenovirus attachment protein, fibre. Both proteins are trimers with head-and-tail morphology. They share unique domain structures and functional properties including defined regions of flexibility within the tail and an unusual symmetry mismatch with the pentameric viral capsid protein into which they are inserted. Moreover, the receptors for reoviruses and adenoviruses, junctional adhesion molecule 1 and coxsackievirus and adenovirus receptor, respectively, also share key structural and functional properties. Although reoviruses and adenoviruses belong to different virus families and have few

properties in common, the observed similarities between signal and fibre point to a conserved mechanism of attachment and an ancient evolutionary relationship. Copyright 2003 John Wiley & Sons, Ltd. (66 Refs.)

Record Date Created: 20030310

Record Date Completed: 20030425

8/7/20

DIALOG(R)File 155:MEDLINE(R)

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11427447 98309961 PMID: 9645993

Coxsackie B virus and its interaction with permissive host cells.

Selinka H C; Huber M; Pasch A; Klingel K; Aepinus C; Kandolf R

Department of Molecular Pathology, University of Tübingen, Germany.

hans-christoph.selinka@med.uni-tuebingen.de

Clinical and diagnostic virology (NETHERLANDS) Apr 1998, 9 (2-3)

p115-23, ISSN 0928-0197 Journal Code: 9309653

Document type: Journal Article; Review; Review, Tutorial

Language: ENGLISH

Main Citation Owner: NLM

Record type: Completed

BACKGROUND: Observations in humans and the results of experiments on laboratory animals have provided evidence that coxsackieviruses of group B (CVB) are major etiologic agents of acute and chronic enterovirus myocarditis and various other virus-induced diseases. **OBJECTIVE:** This minireview briefly summarizes the investigations to elucidate various molecular mechanisms for the induction and maintenance of persistent CVB infections. With regard to the recent findings that CVB may use several different receptor proteins, this article focuses on virus-host cell interactions and the potential impact of these interactions for enteroviral replication. **STUDY DESIGN:** The interaction of CVB with specific cell surface proteins was analyzed in cultured cell lines and murine tissues at the level of virus attachment and virus internalization. As example for the interaction of CVB with intracellular proteins, the state of p21rasGTPase-activating protein (RasGAP) was investigated in mock-infected and CVB3-infected HeLa cells. **RESULTS AND CONCLUSIONS:** The experiments to elucidate the virus receptor interactions revealed the necessity to differentiate between CVB attachment proteins and proteins involved in virus internalization. Since more than one protein may be required to initiate the uptake of CVB into permissive host cells, a model of the putative interaction of these proteins within a multimeric receptor complex is proposed. It is further tempting to speculate that the presence of multiple attachment proteins may influence the tissue tropism of CVB as well as pathogenicity. (39 Refs.)

Record Date Created: 19980916

Record Date Completed: 19980916

8/7/26

DIALOG(R)File 155:MEDLINE(R)

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11085523 9740728 PMID: 9294931

Identification and biology of cellular receptors for the coxsackie B viruses group.

Kuhn R J

Department of Biological Sciences, Purdue University, West Lafayette, Indiana 47907, USA.

Current topics in microbiology and immunology (GERMANY) 1997, 223 p209-26, ISSN 0070-217X Journal Code: 0110513

Document type: Journal Article; Review; Review Literature

Language: ENGLISH

Main Citation Owner: NLM

Record type: Completed

(65 Refs.)

Record Date Created: 19971022

Record Date Completed: 19971022

8/7/47

DIALOG(R)File 155:MEDLINE(R)

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09588865 21372597 PMID: 11479928

Receptor for the group B coxsackieviruses and adenoviruses: CAR.

Carson S D

Department of Pathology and Microbiology, University of Nebraska Medical Center, Omaha, NE 68198-6495, USA. scarson@unmc.edu

Reviews in medical virology (England) Jul-Aug 2001, 11 (4) p219-26, ISSN 1052-9276 Journal Code: 9112448

Document type: Journal Article; Review; Review, Tutorial

Language: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Considerable progress towards the characterisation of the long-sought receptor, CAR (coxsackievirus and adenovirus receptor), shared by group B coxsackieviruses (CVB) and most adenoviruses (Ad) has been made since it was isolated and cloned in 1997. The primary sequence of CAR shows that it is a member of the immunoglobulin superfamily of proteins, containing two Ig superfamily domains: an amino-terminal V-like module and a C2-like module. The CAR cytoplasmic domain, representing nearly one-third of the protein, is separated from the C2-like module by a single membrane-spanning sequence. The structure of the CAR V-like module complexed with the Ad fibre knob has been determined using recombinant proteins, and reveals three CAR modules associated with a single knob. Although recombinant CAR expressed in mammalian cells confers permissivity to CVB infection, details of the interaction between CAR and CVB remain to be elucidated. The expression of CAR appears to be highly regulated with respect to both cell type and developmental age. In rodents, CAR is expressed at high levels

just before birth, and declines thereafter. Expressed levels have been found to increase in regenerating muscle and in response to immunological mediators or inflammation, and in RD cells and umbilical vein endothelial cells in response to high cell density. These studies indicate that CAR expression is highly regulated, but the mechanisms and molecules that mediate the expression remain to be discovered. The physiological function of CAR and its natural ligand also remain to be discovered. In addition, while CAR expression generally correlates with viral tropism, the relationship between the physiological function of CAR and the pathologies of CVB and Ad infections remain to be described. Copyright 2001 John Wiley & Sons, Ltd. (45 Refs.)

Record Date Created: 20010731
Record Date Completed: 20020404

8/7/53

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.
09098690 20396567 PMID: 10936081

Cell receptors involved in adenovirus entry.

Nemerow G R

Department of Immunology, Scripps Research Institute, La Jolla, California 92037, USA. gnemerow@scripps.edu

Virology (UNITED STATES) Aug 15 2000, 274 (1) p1-4, ISSN 0042-6822
Journal Code: 0110674

Contract/Grant No.: EY11431; EY; NEI; HL54352; HL; NHLBI

Document type: Journal Article; Review; Review, Tutorial

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

(18 Refs.)

Record Date Created: 20000925

Record Date Completed: 20000925

8/7/54

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.
09016780 20310108 PMID: 10851559

[Cell receptors for human adenoviruses]

Recepteurs cellulaires des adenovirus humains.

Boulangier P

Laboratoire de Virologie et Pathogenese Moleculaire, Faculte de Medecine de Montpellier, CNRS UMR 5812, Montpellier.

Journal de la Societe de biologie (FRANCE) 1999, 193 (1) p77-84,
Journal Code: 100890617

Document type: Journal Article; Review; Review, Tutorial ; English
Abstract

Languages: FRENCH

Main Citation Owner: NLM

Record type: Completed

During the early stage of the adenovirus infection, the virion binds to a "primary receptor" on the host cell plasma membrane via the fibre projection jutting out of the penton base capsomers located at the twelve apices of the icosahedral capsid. The second step consists of a receptor-mediated endocytosis which involves membrane integrin molecules (the "secondary receptors") and the RGD and/or LDV motifs of penton base. The latter step is inhibited at low temperature, whereas virus attachment to its primary receptor is temperature-independent. Two different primary receptors with a high affinity for the Adenovirus have been recently identified. One is common to Coxsackievirus B3 and adenovirus (CAR), the other one corresponds to a conserved region of the alpha-2 domain of the heavy chain of the major histocompatibility complex class I molecules (MHC-I-alpha 2), overlapping tryptophane-167. The receptor usage by the virus is governed by both cellular and viral parameters. On the cellular side, the relative abundance of one versus the other type of primary receptors would theoretically determine the virus choice. CAR receptor has been mainly found in tissues from mesodermic origin, whereas MHC-I-alpha 2 is ubiquitous. On the virus side, the molecular determinants of the receptor usage have been mapped to the terminal knob of the fibre projection, and have been found to be different for CAR and MHC-I-alpha 2. CAR recognizes linear motifs in fiber knobs in a subgroup-dependent manner, as it binds to all Adenovirus serotypes except for the subgroup B members. MHC-I-alpha 2 however recognizes conformational epitopes carried by fiber knobs from all serotypes tested including subgroup B members. These results should have significant implications in the cell targeting of adenoviral vectors used in gene therapy. (56 Refs.)

Record Date Created: 20000630
Record Date Completed: 20000630
? t s127/21 22
127/21

DIALOG(R)File 155:MEDLINE(R)

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07367084 92230251 PMID: 1566586

A single point mutation of the influenza C virus glycoprotein (FIEF) changes the viral receptor-binding activity.

Szepanski S; Gross H J; Brossmer R; Klenk H D; Hertler G
Institut für Virologie, Philipps-Universität Marburg, Germany.

Virology (UNITED STATES) May 1992, 188 (1) p85-92, ISSN 0042-6822
Journal Code: 0110674

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

From strain JHB/1/66 of influenza C virus a mutant was derived with a change in the cell tropism. The mutant was able to grow in a subline of

Madin-Darby canine kidney cells (MDCK II) which is resistant to infection by the parent virus due to a lack of receptors. Inactivation of cellular receptors by either neuraminidase or acetyltransferase and generation of receptors by resialylation of cells with N-acetyl-9-O-acetylneuraminic acid (Neu5,9Ac2) indicated that 9-O-acetylated sialic acid is a receptor determinant for both parent and mutant virus. However, the mutant required less Neu5,9Ac2 on the cell surface for virus attachment than the parent virus. The increased binding efficiency enabled the mutant to infect cells with a low content of 9-O-acetylated sialic acid which were resistant to the parent virus. By comparing the nucleotide sequences of the glycoprotein (HEF) genes of the parent and the mutant virus only a single point mutation could be identified on the mutant gene. This mutation at nucleotide position 872 causes an amino acid exchange from threonine to isoleucine at position 284 on the amino acid sequence. Sequence similarity with a stretch of amino acids involved in the receptor-binding pocket of the influenza A hemagglutinin suggests that the mutation site on the influenza C glycoprotein (HEF) is part of the receptor-binding site.

Record Date Created: 19920515
Record Date Completed: 19920515

12/7/22

DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.
06152964 89168410 PMID: 2538240

Viral receptors of the immunoglobulin superfamily.

White J M; Litman D R

Department of Pharmacology, University of California, San Francisco 94143.

Cell (UNITED STATES) Mar 10 1989, 56 (5) p725-8, ISSN 0092-8674

Journal Code: 0413066

Document type: Journal Article; Review; Review, Tutorial

Language: ENGLISH

Main Citation Owner: NLM

Record type: Completed

(18 Refs.)

Record Date Created: 19890425

Record Date Completed: 19890425

715197/5

197/5

DIALOG(R)File 155:MEDLINE(R)

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14198605 22326847 PMID: 12438620

Mutations in the N-terminal domains of necrin-1 and necrin-2 reveal differences in requirements for entry of various alphaherpesviruses and for necrin-necrin interactions.

Struyf Frank; Martinez Wanda M; Spear Patricia G; et al

Department of Microbiology-Immunology, The Feinberg School of Medicine,

Northwestern University, 320 E. Superior Street, Chicago, IL 60611, USA.
Journal of virology (United States) Dec 2002, 76 (24) p12940-50,
ISSN 0022-538X Journal Code: 0113724

Contract/Grant No.: F32 GM 19765; GM; NIGMS; R01 AI 49394; AI; NIAID; R37 AI 36293; AI; NIAID; +

Document type: Journal Article

Language: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Necrin-1 and necrin-2 are related molecules that can function with different specificities as entry receptors for mammalian alphaherpesviruses through interaction with viral glycoprotein D (gD). The normal function of members of the necrin family is to mediate cell-cell adhesion through homotypic and heterotypic necrin-necrin interactions in cadherin-based adherens junctions. We examined mutations in three equivalent regions of the N-terminal V-like domains of necrin-1 and necrin-2 to test the effects on entry of various alphaherpesviruses, necrin-necrin interactions, and interactions of the mutant necrins with gD. Mutations in region I previously shown to severely impair herpes simplex virus (HSV) entry activity, but not pseudorabies virus (PRV) or bovine herpesvirus 1 (BHV-1) entry, did not reduce homotypic trans interactions for either necrin-1 or necrin-2 or binding of necrin-3 to necrin-1. Mutations in region II, patterned after a reported single-nucleotide polymorphism in necrin-2, enhanced intracellular accumulation of both necrin-1 and necrin-2 and had a deleterious effect on all of the activities under study. Mutations in region III previously shown to reduce homotypic trans interactions of necrin-2 impaired the entry of PRV and BHV-1 when introduced into either necrin-1 or necrin-2, but only the necrin-2 mutation reduced HSV entry activity. Binding of necrin-1 to necrin-3 was not affected. Effects of the necrin-1 and necrin-2 mutations on interactions with gD did not necessarily correlate with entry activity of the mutant receptors. We can conclude that structural requirements for HSV entry, PRV and BHV-1 entry, and homotypic and heterotypic trans interactions are all different despite the previously reported ability of HSV and HSV gD to inhibit trans interactions.

Record Date Created: 20021119

Record Date Completed: 20021219

? log hold

14may03 11:45:53 User208669 Session D2288.2

\$12.26 3.832 DialUnits File155

\$0.00 154 Type(s) in Format 6

\$2.31 11 Type(s) in Format 7

\$2.31 165 Types

\$14.57 Estimated cost File155

\$6.30 TELNET

\$20.87 Estimated cost this search

\$21.15 Estimated total session cost 3.913 DialUnits

Logoff: level 02.14.01 D 11:45:54

? b 155,357

28aug02 09:50:03 User208669 Session D2092.2

\$0.12 0.037 DialUnits File155

\$0.12 Estimated cost File155

\$0.30 0.037 DialUnits File359

\$0.30 Estimated cost File359

OneSearch, 2 files, 0.074 DialUnits FileOS

\$0.01 TELNET

\$0.43 Estimated cost this search

\$0.78 Estimated total session cost 0.172 DialUnits

SYSTEM: OS - DIALOG OneSearch

File 155: MEDLINE(R) 1966-2002/Aug W4

*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 357: Derwent Biotech Res. 1982-2002/June W1

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*File 357: File enhancements now online. See HELP NEWS 357.

Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description

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? ds

Set Items Description

S1 206 COXSACKIE AND RECEPTOR

S2 220222 TERMINUS OR TERMINAL

S3 9 S1 AND S2

S4 156542 DOMAIN OR DOMAINS

S5 38 S1 AND S4

S6 29 RD (unique items)

? t s3/7/2

3/7/2 (Item 2 from file: 155)

DIALOG(R)File 155: MEDLINE(R)

11290763 21326079 PMID: 11316797

Multiple regions within the coxsackievirus and adenovirus receptor cytoplasmic domain are required for basolateral sorting.

Cohen C J, Gaetz J, Ohman T, Bergelson J M

Division of Immunologic and Infectious Diseases, The Children's Hospital of Philadelphia, Philadelphia, PA 19104-4318, USA. cohenc@email.chop.edu

Journal of biological chemistry (United States) Jul 6 2001, 276 (27)

p25392-8, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: HL54734; HL; NHLBI; T32 AI07278; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The coxsackievirus and adenovirus receptor (CAR) mediates attachment and

infection by coxsackie B viruses and many adenoviruses. In human airway epithelia, as well as in transfected Madin-Darby canine kidney cells, CAR is expressed exclusively on the basolateral surface. Variants of CAR that lack the cytoplasmic domain or are attached to the cell membrane by a glycosylphosphatidylinositol anchor are expressed on both the apical and basolateral surfaces. We have examined the localization of CAR variants with progressive truncations of the cytoplasmic domain, as well as with mutations that ablate a potential PDZ (PSD95/dlg/ZO-1) interaction motif and a putative tyrosine-based sorting signal. In addition, we have examined the targeting of two murine CAR isoforms, with different C-terminal sequences. The results suggest that multiple regions within the CAR cytoplasmic domain contain information that is necessary for basolateral targeting.

Record Date Created: 20010702

? t s6/7/7 15 17 22 27

6/7/7 (Item 7 from file: 155)

DIALOG(R)File 155: MEDLINE(R)

12604321 21547769 PMID: 11688979

Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor.

Thoelen I, Keyaerts E, Lindberg M, Van Ranst M

Laboratory of Clinical and Epidemiological Virology, University of Leuven, Belgium.

Biochemical and biophysical research communications (United States) Nov 9 2001, 288 (4) p805-8, ISSN 0006-291X Journal Code: 0372516

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Non-human adenoviruses such as bovine adenovirus type 3 (BAV-3) that do not replicate in human cells but can infect human cells in culture could provide an attractive alternative to human adenoviral vectors for gene therapy. In addition, a large-animal model for genetic diseases can be very useful for the assessment of the efficacy of adenovector-mediated gene delivery in man. Recombinant human subgroup C adenovectors use the coxsackie and adenovirus receptor (CAR) to enter their target cells.

Through RT-PCR and sequencing we determined the complete coding sequence of bovine CAR which serves as the primary adenoviral attachment site on bovine cells. A multiple sequence alignment, involving all the previously identified CAR species (man, mouse, rat, pig, and dog) showed that bovine CAR was most related to porcine CAR (92% nucleotide similarity) and demonstrated a highly conserved adenovirus binding Ig1 domain. Copyright 2001 Academic Press.

Record Date Created: 20011105

6/7/15 (Item 15 from file: 155)

DIALOG(R)File 155: MEDLINE(R)

11071013 21093138 PMID: 11177539

Manipulation of the cytoplasmic and transmembrane domains alters cell surface levels of the coxsackie-adenovirus receptor and changes the efficiency of adenovirus infection.

van't Hof W; Crystal R G

Division of Pulmonary and Critical Care Medicine, Weill Medical College of Cornell University, New York, NY 10021, USA.

Human gene therapy (United States) Jan 1 2001, 12 (1) p25-34, ISSN 1043-0342 Journal Code: 9008950

Contract/Grant No.: HL51746-06A1; HL; NHLBI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Expression of the coxsackie-adenovirus receptor (CAR) is a critical determinant in cellular susceptibility to infection with adenovirus-based gene transfer vectors. This study is focused on the hypothesis that manipulation of the cytoplasmic tail and transmembrane regions of CAR can be used to change cell surface levels of CAR and, consequently, to alter the efficiency of Ad-mediated gene transfer. To accomplish this, Flag-tagged ([F]) human CAR ([F]CAR), [F]tailless-CAR (lacking the cytoplasmic tail), and [F]GPI-CAR (containing a GPI lipid anchor instead of the transmembrane and cytoplasmic regions) were exogenously expressed in CHO cells. Analysis of (125I)-labeled anti-Flag antibody binding to transfected cells revealed that [F]tailless-CAR and [F]GPI-CAR were expressed on the cell surface in 1.8- to 2.5-fold higher amounts than [F]CAR, while the total expression levels were similar. Infection with replication-deficient adenovirus encoding beta-galactosidase (Ad-betaGal) demonstrated 1.5- to 2-fold higher levels of transgene expression in CHO cells expressing [F]tailless-CAR or [F]GPI-CAR, respectively, compared with cells containing [F]CAR. The form of CAR expressed did not affect the transport of fluorescent Cy3-Ad particles from the cell surface to the nuclear region. These observations indicate that transduction of target cells by Ad vectors can be optimized by increasing cell surface levels of CAR through functional deletion of the tail and membrane protein domains.

Record Date Created: 20010222

6/7/17 (Item 17 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

10511152 20036898 PMID: 10567268

Structural analysis of the mechanism of adenovirus binding to its human cellular receptor, CAR.

Bewley M C; Springer K; Zhang Y B; Freimuth P; Flanagan J M

Biology Department, Brookhaven National Laboratory, Upton, NY 11973, USA. Science (UNITED STATES) Nov 19 1999, 286 (5444) p1579-83, ISSN 0036-8075 Journal Code: 0404511

Contract/Grant No.: 1P41 RR12408-01A1; RR; NCR

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Binding of virus particles to specific host cell surface receptors is known to be an obligatory step in infection even though the molecular basis for these interactions is not well characterized. The crystal structure of the adenovirus fiber knob domain in complex with domain I of its human cellular receptor, coxsackie and adenovirus receptor (CAR), is presented here. Surface-exposed loops on knob contact one face of CAR, forming a high-affinity complex. Topology mismatches between interacting surfaces create interfacial solvent-filled cavities and channels that may be targets for antiviral drug therapy. The structure identifies key determinants of binding specificity, which may suggest ways to modify the tropism of adenovirus-based gene therapy vectors.

Record Date Created: 19991209

6/7/22 (Item 22 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

10092971 99077161 PMID: 9862345

CTX, a *Xenopus* thymocyte receptor, defines a molecular family conserved throughout vertebrates.

Chretien J; Marcuz A; Courtet M; Kavevuo K; Vainio O; Heath J K; White S J; Du Pasquier L

Basel Institute for Immunology, Switzerland.

European journal of immunology (GERMANY) Dec 1998, 28 (12) p4094-104, ISSN 0014-2980 Journal Code: 1273201

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

CTX, a cortical thymocyte marker in *Xenopus*, is an immunoglobulin superfamily (IgSF) member comprising one variable and one constant C2-type IgSF domain, a transmembrane segment and a cytoplasmic tail. Although resembling that of the TCR and immunoglobulins, the variable domain is not encoded by somatic rearrangement of the gene but by splicing of two half-domain exons. The C2 domain, also encoded by two exons, has an extra pair of cysteines. The transmembrane segment is free of charged residues, and the cytoplasmic tail (70 amino acids) contains one tyrosine and many glutamic acid residues. ChT1, a chicken homologue of CTX, has the same structural and genetic features, and both molecules are expressed on the thymocyte surface. We cloned new mouse (CTM) and human (CTH) cDNA and genes which are highly homologous to CTX/ChT1 but not lymphocyte specific. Similarity with recently described human cell surface molecules, A33 antigen and CAR (coxsackie and adenovirus 5 receptor), and a number of expressed sequence tags leads us to propose that CTX defines a novel subset of the IgSF, conserved throughout vertebrates and extending beyond the

immune system. Strong homologies within vertebrate sequences suggest that the V and C2 CTX domains are scions of a very ancient lineage.

Record Date Created: 19990105

6/7/27 (Item 5 from file: 357)

DIALOG(R)File 357:Derwent Biotech Res.

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0256200 DBA Accession No.: 2000-10690

Ectodomain of coxsackie virus and adeno virus receptor genetically fused to epidermal growth factor mediates adeno virus targeting to epidermal growth factor receptor-positive cells - human adeno virus vector cell targeting improvement by epidermal growth factor and coxsackie virus and adeno virus receptor fusion protein for improved gene therapy

AUTHOR: Dmitriev I; Kashitseva E; Rogers B E; Krasnykh V; +Curriel D T
CORPORATE AFFILIATE: Univ.Alabama

CORPORATE SOURCE: Division of Human Gene Therapy, Dept. of Medicine, Pathology and Surgery, Gene Therapy Center, University of Alabama at Birmingham, 1824 6th Ave., South Room WTI 620, Birmingham, AL 35294-3300, USA. email:david.curriel@ccc.uab.edu

JOURNAL: J.Virol. (74, 15, 6875-84) 2000

ISSN: 0022-538X CODEN: JOVIAM

LANGUAGE: English

ABSTRACT: Use of adeno virus (AV) vectors for gene therapy is limited by low efficiency of AV-mediated gene transfer to target cells expressing marginal levels of AV fiber receptor. AV vectors could be improved by modifying AV tropism to target the virus to specific organs/tissues. The fact that the coxsackie virus and AV receptor (CAR) does not play a role in virus internalization, but acts as the virus attachment site, suggests that the extracellular part of CAR may be used to block the receptor recognition site of the AV fiber knob domain. Bispecific fusion proteins may be designed by a recombinant soluble form of truncated CAR (sCAR) and a targeting ligand. sCAR was genetically fused with human epidermal growth factor (EGF) and studied with respect to its ability to target AV infection to the EGF receptor overexpressed on cancer cell lines. sCAR-EGF protein bound to AV virions and directed them to EGF receptor, thereby achieving targeted delivery of reporter gene. sCAE-EGF protein is able to retarget AV via a non-CAR pathway, with attachment of gene transfer efficiency. (55 ref)

? log hold

28aug02 09:58:35 User208669 Session D2092.3

\$2.82 0.881 DialUnits File155

\$0.00 28 Type(s) in Format 6

\$1.05 5 Type(s) in Format 7

\$1.05 33 Types

\$3.87 Estimated cost File155

\$4.03 0.236 DialUnits File357

\$0.00 10 Type(s) in Format 6

\$2.70 1 Type(s) in Format 7

\$2.70 11 Types

\$6.73 Estimated cost File357

OneSearch, 2 files, 1.117 DialUnits FileOS

\$1.95 TELNET

\$12.55 Estimated cost this search

\$13.33 Estimated total session cost 1.289 DialUnits

Logoff: level 02.08.23 D 09:58:35

Reconnected in file OS 28aug02 10:28:19

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2002/Aug W4

*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 357:Derwent Biotech Res. 1982-2002/June W1

(c) 2002 Thomson Derwent & ISI

*File 357: File enhancements now online. See HELP NEWS 357.

Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description

--- -----

? ds

Set Items Description

S1 206 COXSACKIE AND RECEPTOR

S2 220222 TERMINUS OR TERMINAL

S3 9 S1 AND S2

S4 156542 DOMAIN OR DOMAINS

S5 38 S1 AND S4

S6 29 RD (unique items)

S7 159047 CYTOPLASM?

S8 14 S1 AND S7

? log hold

28aug02 10:30:02 User208669 Session D2092.4

\$0.90 0.282 DialUnits File155

\$0.00 10 Type(s) in Format 6

\$0.00 10 Types

\$0.90 Estimated cost File155

\$1.36 0.080 DialUnits File357

\$0.00 4 Type(s) in Format 6

\$0.00 4 Types

\$1.36 Estimated cost File357

OneSearch, 2 files, 0.361 DialUnits FileOS

\$0.43 TELNET

\$2.69 Estimated cost this search

\$2.69 Estimated total session cost 0.361 DialUnits

Logoff: level 02.08.23 D 10:30:02

? b 155,357

28aug02 11:02:35 User208669 Session D2093.1

\$0.28 0.081 DialUnits File1

\$0.28 Estimated cost File1

\$0.01 TELNET

\$0.29 Estimated cost this search

\$0.29 Estimated total session cost 0.081 DialUnits

SYSTEM: OS - DIALOG OneSearch

File 155: MEDLINE(R) 1966-2002/Aug W4

*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 357: Derwent Biotech Res. 1982-2002/June W1

(c) 2002 Thomson Derwent & ISI

*File 357: File enhancements now online. See HELP NEWS 357.

Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description

? s acvvp

S1 1 ACVVP

? t s177/1

1/7/1 (Item 1 from file: 357)

DIALOG(R) File 357: Derwent Biotech Res.

(c) 2002 Thomson Derwent & ISI. All rts. reserv.

0242449 DBA Accession No.: 1999-13214 PATENT

Isolated and purified polynucleotide useful for treating or preventing cancer, inflammation and virus disorders - recombinant virus-receptor protein production via vector-mediated gene transfer and expression in host cell for diagnosis, prevention, therapy and gene therapy

AUTHOR: Lal P, Corley N C

CORPORATE SOURCE: Palo Alto, CA, USA.

PATENT ASSIGNEE: Incyte-Pharm. 1999

PATENT NUMBER: US 5942606 PATENT DATE: 19990824 WPI ACCESSION NO.:

1999-493538 (1941)

PRIORITY APPLIC. NO.: US 979424 APPLIC. DATE: 19971124

NATIONAL APPLIC. NO.: US 979424 APPLIC. DATE: 19971124

LANGUAGE: English

ABSTRACT: An isolated and purified polynucleotide (I) which encodes a protein with the virus-receptor protein (ACVVP) sequence of 390 amino acids (specified), is new. Also claimed are: a composition containing (I); an isolated and purified polynucleotide fully complementary to (I); an isolated and purified polynucleotide (III); an isolated and purified polynucleotide fully complementary to (III); an expression

vector containing (I); a host cell transformed with the expression vector; and a method for detecting (I) in a biological sample containing nucleic acids, which consists of hybridizing the polynucleotide to the nucleic acids of the biological sample to form a hybridization complex and detecting the presence of the hybridization complex, therefore indicating the presence of the polynucleotide which encodes the protein in the sample. The administration of a vector which expressed a polynucleotide which is fully complementary to (I) may be useful for the prevention or treatment of cancer, a virus disorder or inflammation. The polynucleotides which encode ACVVP may be useful for diagnostic purposes and the expression vectors which encode ACVVP may be used for gene delivery. (28pp)

? b 155, 5

28aug02 11:03:18 User208669 Session D2093.2

\$0.21 0.066 DialUnits File155

\$0.21 Estimated cost File155

\$3.97 0.233 DialUnits File357

\$0.00 1 Type(s) in Format 6

\$2.70 1 Type(s) in Format 7

\$2.70 2 Types

\$6.67 Estimated cost File357

OneSearch, 2 files, 0.299 DialUnits FileOS

\$0.21 TELNET

\$7.09 Estimated cost this search

\$7.38 Estimated total session cost 0.380 DialUnits

SYSTEM: OS - DIALOG OneSearch

File 155: MEDLINE(R) 1966-2002/Aug W4

*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 5: Biosis Previews(R) 1969-2002/Aug W4

(c) 2002 BIOSIS

*File 5: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

Set Items Description

? ds

Set Items Description

S1 412 AU=LAL P?

S2 236 AU=CORLEY N?

S3 113 S1 AND S2

S4 940879 RECEPTOR

S5 4 S3 AND S4

S6 10480 CAR OR (COXSACKIE AND RECEPTOR?)

S7 110 HCAR OR MCAR

S8 10542 S6 OR S7

S9 397164 HOMOLOG?
 S10 186 S9 AND S8
 S11 134 RD (unique items)
 S12 60 S4 AND S11
 ?ts5/7/3

5/7/3 (Item 3 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)

(c) 2002 BIOSIS. All rts. reserv.

12195930 BIOSIS NO.: 199900490779

Viral receptor protein.

AUTHOR: Lal Preeti(a); Corley Neil C

AUTHOR ADDRESS: (a)VISX Inc., Santa Clara, CA**USA

JOURNAL: Official Gazette of the United States Patent and Trademark Office

Patents 1225 (4):pNO PAGINATION Aug. 24, 1999

ISSN: 0098-1133

DOCUMENT TYPE: Patent

RECORD TYPE: Citation

LANGUAGE: English

? log hold

28aug02 11:07:46 User208669 Session D2093.3

\$3.78 1.180 DialUnits File155

\$0.00 61 Type(s) in Format 6

\$0.00 61 Types

\$3.78 Estimated cost File155

\$4.88 0.871 DialUnits Files

\$0.00 13 Type(s) in Format 6

\$1.75 1 Type(s) in Format 7

\$1.75 14 Types

\$6.63 Estimated cost Files

OneSearch, 2 files, 2.051 DialUnits FileOS

\$1.08 TELNET

\$11.49 Estimated cost this search

\$18.87 Estimated total session cost 2.431 DialUnits

Logoff: level 02.08.23 D 11:07:46

OM protein - protein search, using sw model

Run on: August 19, 2002, 16:13:17 ; Search time 57.91 Seconds
(without alignments)

updates/sec 748.036 Million cell

Title: US-09-902-759-39

Perfect score: 2012
Sequence: 1 MISLPGPLVTNLLRFLFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

1: /SIDS1/gcgdata/hold-geneseq/geneeqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneeqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneeqp-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/hold-geneseq/geneeqp-emb1/AA1983.DAT:*
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16: /SIDS1/gcgdata/hold-geneseq/geneeqp-emb1/AA1995.DAT:*
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18: /SIDS1/gcgdata/hold-geneseq/geneeqp-emb1/AA1998.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneeqp-emb1/AA1999.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneeqp-emb1/AA2000.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|--------|----------------|--------|----|----------|--------------------|
| 1 | 2012 | 100.0 | 390 | 20 | AAV27096 | Human viral recept |
| 2 | 2012 | 100.0 | 390 | 20 | AAV13351 | Amino acid sequenc |
| 3 | 2012 | 100.0 | 390 | 20 | AAV05286 | EGF-like homologue |
| 4 | 2012 | 100.0 | 390 | 21 | AAV88574 | Human PRO246 amino |
| 5 | 2012 | 100.0 | 390 | 21 | AAV94999 | Human secreted pro |
| 6 | 2012 | 100.0 | 390 | 22 | AAV12340 | Human PRO246 polyP |
| 7 | 2012 | 100.0 | 390 | 22 | AAV88358 | Human membrane or |
| 8 | 2012 | 100.0 | 390 | 22 | AAV68599 | PRO246. Homo sapi |
| 9 | 2012 | 100.0 | 390 | 22 | AAV31207 | Amino acid sequenc |
| 10 | 2012 | 100.0 | 390 | 22 | AAV80219 | Human PRO246 prote |
| 11 | 2012 | 100.0 | 390 | 22 | AAV53082 | Human angiogenesis |
| 12 | 2004 | 99.6 | 390 | 22 | AAE06610 | Human protein havi |
| 13 | 2004 | 99.6 | 390 | 22 | AAV90818 | Human shear stress |
| 14 | 2003 | 99.6 | 389 | 21 | AAV76303 | Fragment of human |
| 15 | 1738.5 | 86.4 | 370 | 22 | AAV65832 | Human INTERCEPT |
| 16 | 1736.5 | 86.3 | 370 | 22 | AAV65906 | Human secreted pro |
| 17 | 1734.5 | 86.2 | 370 | 22 | AAV65904 | Human secreted pro |
| 18 | 1734.5 | 86.2 | 370 | 22 | AAV65905 | Human secreted pro |
| 19 | 1734.5 | 86.2 | 370 | 22 | AAV65907 | Human secreted pro |
| 20 | 1601.5 | 79.6 | 341 | 22 | AAV65833 | Murine mature INTE |
| 21 | 1581 | 78.6 | 321 | 22 | AAV11937 | Human viral recept |
| 22 | 1581 | 78.6 | 321 | 22 | AAV40551 | Human polypeptide |
| 23 | 1579 | 78.5 | 325 | 21 | AAV95024 | Human clone vcs1_1 |
| 24 | 1399 | 69.5 | 394 | 22 | AAV65910 | Murine secreted pr |
| 25 | 1397 | 69.4 | 394 | 22 | AAV65840 | Murine secreted pr |
| 26 | 1397 | 69.4 | 394 | 22 | AAV65908 | Murine secreted pr |
| 27 | 1394 | 69.3 | 394 | 22 | AAV65911 | Murine secreted pr |
| 28 | 1393 | 69.2 | 394 | 22 | AAV65909 | Murine secreted pr |
| 29 | 1331 | 66.2 | 365 | 22 | AAV65841 | Murine mature INTE |
| 30 | 1232 | 61.2 | 246 | 22 | AAV65835 | Murine INTERCEPT |
| 31 | 1207 | 60.0 | 237 | 21 | AAV76152 | Human secreted pro |
| 32 | 1107 | 55.0 | 220 | 22 | AAV65872 | Human INTERCEPT |
| 33 | 1095 | 54.4 | 217 | 22 | AAV65871 | Human INTERCEPT |
| 34 | 1027 | 51.0 | 206 | 22 | AAV65870 | Human INTERCEPT |
| 35 | 965.5 | 48.0 | 212 | 20 | AAV25748 | Human secreted pro |
| 36 | 890 | 44.2 | 177 | 22 | AAV65867 | Human INTERCEPT |
| 37 | 833.5 | 41.4 | 249 | 22 | AAV65843 | Murine INTERCEPT |
| 38 | 833 | 41.4 | 172 | 22 | AAV38765 | Human polypeptide |
| 39 | 577 | 28.7 | 182 | 22 | AAE05354 | Mouse 10.3 kDa pro |
| 40 | 467.5 | 23.2 | 120 | 22 | AAV65846 | Murine INTERCEPT |
| 41 | 436 | 21.7 | 127 | 21 | AAV95025 | Human clone vcs1_1 |
| 42 | 400.5 | 19.9 | 99 | 22 | AAV65837 | Murine INTERCEPT |
| 43 | 400 | 19.9 | 80 | 22 | AAV65838 | Murine INTERCEPT |
| 44 | 367.5 | 18.3 | 426 | 22 | AAV10359 | Human cDNA SEQ ID |
| 45 | 361.5 | 18.0 | 376 | 19 | AAV57213 | Mouse coxsackievir |

ALIGNMENTS

RESULT 1
AAV27096
ID AAV27096 standard; Protein; 390 AA.

XX AC AAY27096;
XX DT 18-OCT-1999 (first entry)
XX DE Human viral receptor protein (ACVRP).
XX KW Viral receptor protein; ACVRP; cancer; viral disorder; inflammation;
XX KM gene therapy; human.
XX OS Homo sapiens.
XX PN US5942606-A.
XX PD 24-AUG-1999.
XX PF 24-NOV-1997; 97US-0979424.
XX PR 24-NOV-1997; 97US-0979424.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Corley NC, Lal P;
XX DR WPI; 1999-493538/41.
XX PS N-PSDB; AAX87000.
XX PT Isolated and purified polynucleotide useful for treating or
XX PT preventing cancer, inflammation and viral disorders
XX PS Claim 1; Fig 1A-D; 28pp; English.
XX CC This represents a human viral receptor protein (ACVRP). The protein
CC can be expressed by standard recombinant methodology. ACVRP can be used
CC for treating and/or preventing cancer, a viral disorder or inflammation
CC through the administration of a vector expressing a polynucleotide which
CC is fully complementary to the present sequence. Polynucleotides encoding
CC ACVRP can be used for diagnostic purposes to quantitate ACVRP expression
CC in biopsied tissues and correlate expression with disease. They can be
CC used to distinguish between the absence, presence and excess expression
CC of ACVRP and to monitor levels during therapeutic intervention.
CC Hybridisation probes can be used for mapping the naturally occurring
CC genomic sequence and detect differences in the chromosomal location in
CC normal, carrier or affected individuals. ACVRP may be ligated to a
CC heterologous sequence to produce a fusion protein which can be used to
CC screen peptide libraries for inhibitors of ACVRP activity and to screen
CC for novel antiprotocol and antifungal therapeutics. The expression
CC vectors which encode ACVRP can be used to deliver nucleotide sequences
CC to targeted organ, tissue or cell populations and complementary
CC polynucleotides to treat conditions associated with overexpression of
CC ACVRP by blocking transcription of the mRNA, modulating ACVRP activity
CC or regulating the gene function.
XX SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 20; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;

Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQQLHLPLANRLQAVEGSEVVLPAWYTLHGEV 60
|||||
Db 1 mislpgplvtcnllrflflglalsalappsraqqlhlpanrlqavegsevvlpawylhgev 60
QY 61 SSSQPEVFPFVWMEFKQEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGIQEKD 120
|||||
Db 61 sssqpevpfvmwffkqekedqvlsyinyngvttskpvslyvsmprnlslrleglqekd 120
QY 121 SGPYSCSVNVODKQKSRGHSIKTLELNVLVPPAPPSCRLOQVPHVGANVTLSQSPRSK 180
|||||
Db 121 sgpyscsvnvodkqksgsrghsiktletnlvlpappscrlqgvphvganvtlscqgsprsk 180
QY 181 PAVQYQWDRQLPSFGTFEAPALDVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCVTLE 240
|||||
Db 181 pavqyqwdrtqlpsfgtffapaldivrsglsstnlssmagyvcakahnevgtacgvltle 240
QY 241 VSTGPGAAVAVGAVVGTLVGTLVGLVLYHRRGKALEBPANDIKEDAIAPRTLPMPPKS 300
|||||
Db 241 vstgpgaaavavavvgvtlvglvlyhrrgkaleebpandikedaiaprtlpmpks 300
QY 301 SDTISKNGTILSSVTSARALRPPHPPRGALTPTPSLSSQALPSPRLPTTGCAHPDIPSP 360
|||||
Db 301 sdtiskngtissvtsaeralpphpprgaltptpslssqalpsprlpttgahpdpisp 360
QY 361 IPGVSSSGSLSRMGAVPVMVPAQSQAGSLV 390
|||||
Db 361 ipgvasssglsrmgavpvmvpaqsgagslv 390

RESULT 2
AAY13351
ID AAY13351 standard; Protein; 390 AA.
XX
AC AAY13351;
XX
DT 25-JUN-1999 (first entry)
XX
DE Amino acid sequence of protein PRO246.
XX
KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
KW anti-thrombotic; wound healing; tissue repair.
XX OS Homo sapiens.
XX PN WO9914328-A2.
XX PD 25-MAR-1999.
XX PF 16-SEP-1998; 98WO-US19330.
XX

PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059113.
PR 17-SEP-1997; 97US-0059115.
PR 17-SEP-1997; 97US-0059117.
PR 17-SEP-1997; 97US-0059119.
PR 17-SEP-1997; 97US-0059121.
PR 17-SEP-1997; 97US-0059122.
PR 17-SEP-1997; 97US-0059184.
PR 18-SEP-1997; 97US-0059263.
PR 18-SEP-1997; 97US-0059266.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 21-OCT-1997; 97US-0063486.
PR 24-OCT-1997; 97US-0062814.
PR 24-OCT-1997; 97US-0062816.
PR 24-OCT-1997; 97US-0063045.
PR 24-OCT-1997; 97US-0063120.
PR 24-OCT-1997; 97US-0063121.
PR 24-OCT-1997; 97US-0063127.
PR 24-OCT-1997; 97US-0063128.
PR 27-OCT-1997; 97US-0063329.
PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063541.
PR 28-OCT-1997; 97US-0063542.
PR 28-OCT-1997; 97US-0063544.
PR 28-OCT-1997; 97US-0063549.
PR 28-OCT-1997; 97US-0063550.
PR 28-OCT-1997; 97US-0063564.
PR 29-OCT-1997; 97US-0063435.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063738.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.
PR 29-OCT-1997; 97US-0063735.
PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.

XX (GETH) GENENTECH INC.

PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

DR MPI, 1999-229533/19.
DR N-PSDB; AAX52221.

XX

PT New isolated human genes and polypeptides used in, e.g. treatment of
PT gastrointestinal ulceration
XX
PS Claim 12; Fig 17; 320pp; English.

CC AA1Y344-403 represent secreted and transmembrane human proteins.
CC The cDNA sequences are obtained from cDNA libraries, prepared from
CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
CC The encoded polypeptides have specific uses based on their homology to
CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
CC associated with the preservation and maintenance of gastrointestinal
CC mucosa and the repair of acute and chronic mucosal lesions
CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
CC ulceration and congenital microvillus atrophy), skin diseases associated
CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
CC potent effects on cell growth and development, diseases related to
CC growth or survival of nerve cells including Parkinson's disease,
CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
CC as a target for anti-tumor drugs. PRO533 may be used in the treatment
CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an
CC anti-thrombotic agent; PRO287 polypeptides and portions may have
CC therapeutic applications in wound healing and tissue repair; PRO317 can
CC be used for treating problems of the kidney, uterus, endometrium, blood
CC vessels, or related tissue, e.g. in the heart of genital tract.

XX Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 20; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MISLPGDLVNLRLFLGLSALAPPSRAQLQHLPANRLQAVEGGEVLPWYTLHGEV 60
|||||

Db 1 mslspgplvtlnlrlflglalslappsrarqqlhpanrlqavegeevlpawtytlhgev 60
|||||

QY 61 SSSQPEVFPFVWMPFKXKEKEQDVLXYINGVTTSKPGVSLVYSPMSRNLRLRLGLEQEKD 120
|||||

Db 61 sssqpevfpfvmwffkxkokedqvlvyingvtstskgvsalvympsrnlrlrlgleqekd 120
|||||

QY 121 SGPYSCSVNVDDKQKSRGHSKITLEANVLVPPAPSCRLQGVPHGANVTLSCQSRSK 180
|||||

Db 121 sgpyscsvnvvdqkgsrghskitleanvlvpappscrlgvpghganvtlscqspbrsk 180
|||||

QY 181 PAVQYOMDRQLPSFQTFAPALDIVRGLSLTNLSSMAGVYVCKAHNEVGTAQCNTLE 240
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181 pavqyqwdrlpsfqtffapaldvigrslsltnlssmagvyvckahnevgtaqcncvtle 240
|||||
Db 241 VSTGPAAVVAGAVGTVLGLIAGLVILVHRGKALKEBPANDIKEDAIAPRTLWPXKS 300
|||||
241 vstgpaavvagavvgtlvgllaglvllvhrgkaleebpandikedaiaprtlwpkps 300
|||||
QY 301 SDTISKNGTSSVTSAKALRPDPHGPFRPGALTPFSLSSQALPSPRLPTTGAAHPDIPSP 360
|||||
301 sdtiskngtssvtsaakalrppdhgpprpgaltptfslssqalpsprlpttgahpdipsp 360
|||||
Db 301 sdtiskngtssvtsaakalrppdhgpprpgaltptfslssqalpsprlpttgahpdipsp 360
|||||

1 QY 361 IPGVSSSSGLSRMGAVPMVPAQSQAGSLV 390
|||||
Db 361 IPGVSSSSGLSRMGAVPMVPAQSQAGSLV 390

RESULT 3

AAV05286

ID AAV05286 standard; Protein; 390 AA.

XX AAV05286;

XX 22-JUN-1999 (first entry)

DE EGF-like homologue PRO246.

XX Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261;
PRO246;

KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;
KW FGF-8 homologue.

XX Homo sapiens.

XX WO914327-A2.

XX 25-MAR-1999.

PF 10-SEP-1998; 98WO-US18824.

PR 25-NOV-1997; 97US-0066840.

PR 17-SEP-1997; 97US-0059114.

PR 17-SEP-1997; 97US-0059117.

PR 18-SEP-1997; 97US-0059263.

PR 15-OCT-1997; 97US-0062125.

PR 17-OCT-1997; 97US-0062285.

PR 17-OCT-1997; 97US-0062287.

PR 24-OCT-1997; 97US-0062816.

PR 29-OCT-1997; 97US-0063704.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;
PI Roy M, Wood WI;

XX WPI; 1999-229532/19.

XX N-PSDB; AAX28436.

XX Antibodies against specific proteins overexpressed in tumours

XX Example 1; Fig 27; 130pp; English.

XX This sequence represents the EGF-like homologue PRO246.

XX The invention relates to antibodies (Ab) that bind to any of the

XX polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211;
CC PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit
CC expression and/or activity of (I) are used: (i) to inhibit growth of
CC tumours; and (ii) as diagnostic/prognostic reagents for detection or
CC quantification of (I) in cells or tissues, by standard immunoassays,
with

CC overexpression being indicative of cancer. For therapeutic use, the Ab
CC may be conjugated to a toxin, chemotherapeutic agent or radioisotope.
CC Genes expressing (I), many of which are growth factor homologues, are
CC overexpressed in some cases of cancer.

XX SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 20; Length 390;

Best Local Similarity 100.0%; Pred. No. 5,8e-143;

Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps

0;

QY 1 MTSLPGLVTNLLRFLFLGLSALAPPSRAQLQLHPANRLQAVEGSEVLPAMYTLHGEV 60

Db 1 mislpplvtlnllrflflglalsaptraqlqhlpanrlqavegevvlpawyltlhgev 60

QY 61 SSSQPEVFPVWMEFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSHLSLRLEGLOEKD 120

Db 61 ssqpwefpvmwffkqkdekdvlsyngvtctskpgvslvympsrnlslrlgldqkd 120

QY 121 SGPYSCSVNVODKQKGRGHSITKLELVLPAPAPSCRLQGVPHGANVTLSQSPRSK 180

Db 121 sgpyscsvnvodkqkgrghsiktlevlpapapscrlgvyphganvltscqsprsk 180

QY 181 PAVQYQMDROLPSQTFPAPALDIVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCNTLE 240

Db 181 pavqyqwdrlpsqtfpapaaldivirgslstnlssmagvyvckahnevtaqcantle 240

QY 241 VSTGPGAAVVAGVGTLVGLGLAGLVLYHRRGKALEEPANDIKEDAIAPRTLPMWPKS 300

Db 241 vstgpgaavvavagvtlvglglaglvlyhrrgkaleepandikedaiaprtlpmpks 300

QY 301 SPTISKNGTLLSVTSARALRPHPGPRRGALTPTPSLSSQALPSRLPTTDGHPQPIPS 360

Db 301 sptiskngtltsvtsaralrphpgpprgaltpptpslssqalpsrpttdghpqpisp 360

QY 361 IPGVSSSSGLSRMGAVPMVPAQSQAGSLV 390

Db 361 IPGVSSSSGLSRMGAVPMVPAQSQAGSLV 390

RESULT 4

AAV88574

ID AAV88574 standard; Protein; 390 AA.

XX AAV88574;

XX 09-AUG-2000 (first entry)

DE Human PRO246 amino acid sequence.

XX Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261;
KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;
KW cell growth; proliferation; cell surface virus receptor; ADDEPT;
KW antibody dependent enzyme mediated prodruq therapy.

OS Homo sapiens.
 XX WO200015666-A2.
 PN
 XX 23-MAR-2000.
 PD
 XX 08-SEP-1999; 99WO-US20594.
 PF
 XX 10-SEP-1998; 98US-0099803.
 PR 10-SEP-1998; 98WO-US18824.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX
 PI Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;
 PI
 XX WPI; 2000-271386/23.
 DR N-PSDB; AAA30052.
 DR
 XX
 PT New isolated antibodies which bind to specific polypeptides used for
 PT diagnosis and treatment of neoplastic cell growth and proliferation -
 XX
 PS Example 8; Fig 16; 200pp; English.
 PS
 XX
 CC This sequence represents a human PRO246 amino acid sequence. PRO246 is
 CC probably a cell surface virus receptor. The invention relates to
 isolated
 CC antibodies which bind to a polypeptide. The "PRO" polypeptides are
 CC encoded by genes which are over expressed in the genome of tumour cells.
 CC Vectors and host cells comprising the nucleic acid encoding the
 CC antibodies are used in the production of the antibodies. The antibodies
 CC and nucleic acids encoding them are used for diagnosing a tumour in a
 CC mammal. The antibodies are used for inhibiting the growth of tumour
 cells
 CC and identifying compounds that inhibit a biological or immunological
 CC activity of and/or expression of a PRO187, PRO533, PRO214, PRO240,
 CC PRO211, PRO230, PRO261, PRO246 or PRO317 polypeptide. The antibody can
 be
 CC used in antibody dependent enzyme mediated prodrug therapy (ADEPT) by
 CC conjugating the antibody to a prodrug-activating enzyme which converts
 a
 CC prodrug to an anti-cancer drug. The antibodies can be fluorescently
 CC labelled and monitored by light microscopy, flow cytometry or
 fluorimetry
 CC for diagnosis and prognosis of tumours.
 XX
 SQ Sequence 390 AA;
 SQ
 Query Match 100.0%; Score 2012; DB 21; Length 390;
 Best Local Similarity 100.0%; Pred. No. 5.8e-143;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
 0;
 QY 1 MISLPGPLVTLNLRFLFLGLSALAPPSRAQQLHLPA NRLOAVEGGEVVLPAWYTLHGEV 60
 Db 1 mislpgplvtnllrlflflglasalapsraqqlhlpanrlqaveggevvlpawytihgev 60
 QY 61 SSSQPMWEVPFVMWFVKQKEKEDQVLSYINGVTTSKPGVSLVYSPSRNLRLLEGIQEKD 120

Db 61 sssqpmwepfvvmwffkqkexkedqvlsyinygttskpgvslyvsmprnlrllegiqekd 120
 QY 121 SGPYSCSVNVODKQGKSRGHSIKTLELNVLVPPAPPSCRLOGVPHVGANVTLSQSPRSK 180
 Db 121 sgpyscsvnvodkqgksrghsiktletnlvlpapppscrlogvphvganvtlsqgsprsk 180
 QY 181 PAVQYQWDRQLPSFQTFEPAPALDIVRGSLSITNLSSMAGVYVCKAHNEVGTAQCNVTLE 240
 Db 181 pavqyqwdrqpsfqtcfepapaldvirgslsitnlssmagvyvckahnevgtacqcnvtle 240
 QY 241 VSTGPGAAVVAGAVVGTLVGLLGLAGLVLLYHRRGKALBEPANDIKEDAIAPRTLPMWPKS 300
 Db 241 vstgpgaavvavagavvgtlvglglaglvlllyhrrgkaleepandikedaiaprtlpwps 300
 QY 301 SDTISKNGTILSSVTSARALRPDPHGP RPFGALPTTPSLSSQALPSPLPTTGAPHPISP 360
 Db 301 sdtiskngtllssvtsaaralrphgpprpfgalpttpslssqalspsrlpttgahpisp 360
 QY 361 IPGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
 Db 361 ipgvsssglsrmgavpvmvpapqsgagslv 390
 RESULT 5
 AAY94999
 ID AAY94999 standard; Protein; 390 AA.
 XX
 AC AAY94999;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Human secreted protein vc51_1, SEQ ID NO:38.
 XX
 KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
 KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
 KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
 KW neurodegenerative disease; asthma; contraceptive.
 XX
 OS Homo sapiens.
 XX
 PN WO200011015-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 24-AUG-1999; 99WO-US19351.
 XX
 XX 24-AUG-1998; 98US-0097638.
 PR 24-AUG-1998; 98US-0097659.
 PR 09-SEP-1998; 98US-0099618.
 PR 28-SEP-1998; 98US-0102092.
 PR 25-NOV-1998; 98US-0109978.
 PR 23-DEC-1998; 98US-0113645.
 PR 23-DEC-1998; 98US-0113646.
 PR 23-AUG-1999; 99US-0379246.
 PA (ALPH-) ALPHAGENE INC.
 XX

PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-224657/19.
XX
PT New secreted or transmembrane proteins and polynucleotides encoding
PT them, useful for treating neurodegenerative disorders, autoimmune
PT diseases and cancer -
XX
PS Claim 47; Page 296-297; 357pp; English.
XX
CC The invention relates to 40 human secreted proteins (AAV94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
CC proteins of the invention include those that are thought to be only
CC partially secreted, i.e., transmembrane proteins. The proteins of the
CC invention may exhibit one or more activities selected from the
CC following:
CC cytokine activity; cell proliferation; differentiation; immune
CC modulation; haematopoiesis regulation; tissue growth activity;
CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
CC and thrombolytic activity; anti-inflammatory activity; and tumour
CC inhibition activity. The proteins may be administered to patients as
CC vaccines, and the nucleotides may be used as part of a gene therapy
CC regime. Diseases or conditions that may be treated using the proteins or
CC nucleotides of the invention include autoimmune diseases; genetic
CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
CC fungal and viral infections, especially HIV; multiple sclerosis;
CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
CC insulin dependent diabetes mellitus; and allergic reactions such as
CC asthma and anaemia. They may also be used for treating wounds, burns,
CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease and amyotrophic
CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may
CC additionally be useful as contraceptives. Nucleic acid sequences of the
CC invention may be used in chromosome mapping, and as a source of
CC diagnostic primers and probes. The present sequence represents one of
CC the
CC 40 proteins of the invention.
CC
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 21; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

QY 1 MISLPGPLVTNLRLFLIGLSALAPPSRAQLQHLPANRLQAVEGGEVVLPAWYTLHGEV 60
DB 1 mislpgplvtntlrlfliglsalappstragqlhlpantlqaveggevvlpawylhgev 60
QY 61 SSSQDWEVFPVMMFVKQKEKDQVLSYINGVTTSKPGVSLVYMSRNLSLRLEGIQEKD 120
DB 61 sssqdwefvpmwffkqkqedqvlsyngvttskpgvslvysmpsrnlslrlleglqekd 120
QY 121 SGPYSCSVNVQDKGKSRGHSIKTELNLVLPAPPSCRILQGVPHVGANVTLSCSPRSK 180
DB 121 sgpyscsvnvqdkgksgrgshsiktelnlvlpappscrilqgvphvganvtlscqgsprsk 180

QY 181 PAVQYQWDRQLPSFQTFPAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE 240
DB 181 pavqyqwdrlpsfqtfpapaldvirgslsltnlssmagyvvcakhnevgtacqcnvtle 240
QY 241 VSTGPGAAVAVGAVVGLTVGLIAGLVLYHRRGKALEEPANDIKEDALPRTLWPMS 300
DB 241 vstgpgaaavavavgltvglilaglvlyhrrgkaleepandikedalprtllwpms 300
QY 301 SDTISKNGTSSVTSARALRPHGPRRGALITPSSLSSQALPSRPLPTDGAHPQIPSP 360
DB 301 sdtiskngtssvtsaaralrphgprrgalitpsslssqalpsrplptdga hpqisp 360
QY 361 IPGVSSSGSLSRMGAVPMVPAQSQAGSLV 390
DB 361 ipgvsssgslsrmgavpmvpaqsgagslv 390

RESULT 6

AAU12340
ID AAU12340 standard; Protein; 390 AA.

XX
AC AAU12340;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO246 polypeptide sequence.

XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal
muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.

XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.

AAU12172AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor- α (TNF- α) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.

```

Db      1 mislpgplvtlnllrrfflfiglslalappaiaqlqhlpanrlgaveggevvlpwactllngev 60
QY      61 SSSQPMWEVPFNWMEFFKQKEKEQOVLSITNGVTTSPGVSLVYSMPSRNLSLRLEGLOEKD 120
        |||
        |||
        |||
Db      61 ssaspwepvflvmwffkqkckedqvlslngvltskpyslvysmpsrnlslrlgldgkd 120
QY      121 SGPPYSCSVNVODKQKSGRSHSIKTLLEINLVPPAPPSCRLOGVPHVGANVTLSQSPRSK 180
        |||
        |||
        |||
Db      121 sgpyscsvnvqdkqgkargshsktelnlvppappscrllgvyphvganvtlscqpsrsk 180
QY      181 PAVQYQWDRQLPSFQTFAPALDIVIRGSLSTNLTSSSMAGVYVCKAHNEVGTAQCNVLE 240
        |||
        |||
        |||
Db      181 pavqyqwdrlpsfqtffapaldvirsislclnlssmagvyvckahnevgaqcnvtle 240
QY      241 VSTPGAAVAVAGAVGTLVGLGLAGLVLYNHRGKALEEPANDIKEDAIAPRTLPMWPKS 300
        |||
        |||
        |||
Db      241 vstpgaaavagavgtlvglglaglvlynhrgkaleepandikedaiaprtlpwps 300
QY      301 SPTISKNGTLSSVTSARALRPHGPBPBGALPTPSSSQALPSRLPTTDGAPQPISP 360
        |||
        |||
        |||
Db      301 sdtskngtllssvtsaralrphgpprpgaloptpslsqalpsrplpttdgahpqpisp 360
QY      361 IPGGVSSSGLSRMGAVPVMPAOSQAGSLV 390
        |||
        |||
        |||
Db      361 ipgvsassglstrmgavpvmvpaqsqagslv 390

RESULT 7
AAB8358
ID      AAB88358 standard; Protein; 390 AA.
XX
AC      AAB88358;
XX
DT      23-MAY-2001 (first entry)
XX
DE      Human membrane or secretory protein clone PSEC0086.
XX
KW      Human; secretory protein; membrane protein; vaccine; gene therapy;
        rheumatoid arthritis; diabetes.
XX
OS      Homo sapiens.
XX
PN      EP1067182-A2.
PD      10-JAN-2001.
XX
PF      07-JUL-2000; 2000EP-0114090.
XX
PR      08-JUL-1999; 99JP-0194179.
PR      11-JAN-2000; 2000JP-0118775.
PR      02-MAY-2000; 2000JP-0183766.
XX
PA      (HELI-) HELIX RES INST.
XX
PI      Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
DR      WPI; 2001-093989/11.
DR      N-PSDB; AAF93785.
OR

```

1
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development -
XX
PS Claim 1; SEQ ID 84; 609pp + CD ROM; English.
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by
CC AAB86317 - AAB86419. Included in the invention are primers
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate
the
CC cDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays
to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies and antagonists may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

QY 1 MISLPGLVTNLTLPFLFLGSLALAPPSRAQLHLIPANRLQAVEGGEVVLPAWYTLHGEV 60
Db 1 mislpglvtlnltlrfllglalsalappstraqlhlipantlqaveggevvlpawylhgev 60
QY 61 SSSQDWEVPVVMWFVKQKEKEDQVLSYINGVTSKPGVSLVSMPSRNLSLRLEGIQEKD 120
Db 61 sssqdwepvvmwvfkrqekedqvlsyinyngvtskpgvslvsmpsrnlslrlleglqekd 120
QY 121 SGPYSCSVNVODKQGRSGHSIKTELNLVLPAPPSCRILQGVPHYGANVTLSCGSPRSK 180
Db 121 sgpyscsvnvodkqgrsghsiktelnlvlpappscrilgvphvganvtlscgqprsk 180
QY 181 PAVOYQWDRQLPSFQTFAPALDVTIRGSLSTNLSSMAGVYVCCAHNVEGTACQCVTLE 240
Db 181 pavgyqwdrlpsfqtffapaldvirgslstnlssmagvyvckahnevgtacqcnvtle 240
QY 241 VSTGPAAVAVGAVVGTLVGLAGLVLLVYHRKGALEBPANDIKEDAIAPRTLWPWPKS 300

Db 241 vstgpgaavvagavvgtlvglaglvllvhyrkgaleebpandikedaiaprtlpwps 300
QY 301 SDTISKNGTSSVTSARALRPHPRPFGALTPTPSISSQALPSRPLPTDGAHPQPISP 360
Db 301 sdtiskngtssvtsaralrpphrpfpfgaltptpslssqalpsrplptdgahpqpi sp 360
QY 361 IPGVSSSGLSRMGAVPMVPAQSQAGSLV 390
Db 361 ipgvsssglsrmgavpmvpaqsqagslv 390

RESULT 8
AAB68599
ID AAB68599 standard; Protein; 390 AA.

AC AAB68599;
XX
DT 27-APR-2001 (first entry)
DE PRO246.
XX
KW Cytostatic; PRO protein; tumour; cancer.
XX
OS Homo sapiens.

XX
PN MO200105836-A1.
XX
PD 25-JAN-2001.
XX
PF 20-DEC-1999; 99WO-US30999.
XX
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28564.

XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
XX
XX WPI; 2001-091968/10.
DR N-PSDB; AAF60372.
DR
XX
PT New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,
PT useful for diagnosing and treating cancers -
XX
PS Claim 61; Fig 16; 196pp; English.
XX
CC The present invention relates to PRO proteins and coding sequences. The
CC present sequence is one such PRO protein. It was found that the PRO
genes
CC are amplified in the genome of tumour cells. The gene amplification is

SQ Sequence 390 AA;

0

Db 1 mislpgplvtcnilrflflglalsalappsrqqlqlhlpanrlgavegevvlpawtllngev 60

Db 61 sssqpwepfvmmffkqkakedqvl syingvtskpgvslvyampsrnlslrlleglqekd 120

Db 121 sgpyscsvnvdkgksrghsikt1elnvlvpappscr1qgvphvganvt1scqsprsk 180

Db 181 pavqywdrqlpsfqtffapaldivrgslsltnlssmagvyvckahnevgtacnvtle 240

Db 241 vstgpaavagavgtlvglglaglvllhnrqka1eepandikedaiaprtlppwps 300

Db 301 sdtlsknqtlssvtsaralrpphpgpprgaltptpslsqalpsprlptcdgahpqpisp 360

361 1pggvsssg1stmgavpvmvpaqsqagslv 390

RESULT 9

ID AAB31207 standard; Protein; 390 AA.

AC AAB31207;

DT 20-APR-2001 (first entry)

DE Amino acid sequence of human polypeptide PRO246.

KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361;

05 Homo sapiens.

| FH | Key | Location/Qualifiers |
|-----|-----|---------------------|
| 1 | 1 | 1 |
| 2 | 2 | 2 |
| 3 | 3 | 3 |
| 4 | 4 | 4 |
| 5 | 5 | 5 |
| 6 | 6 | 6 |
| 7 | 7 | 7 |
| 8 | 8 | 8 |
| 9 | 9 | 9 |
| 10 | 10 | 10 |
| 11 | 11 | 11 |
| 12 | 12 | 12 |
| 13 | 13 | 13 |
| 14 | 14 | 14 |
| 15 | 15 | 15 |
| 16 | 16 | 16 |
| 17 | 17 | 17 |
| 18 | 18 | 18 |
| 19 | 19 | 19 |
| 20 | 20 | 20 |
| 21 | 21 | 21 |
| 22 | 22 | 22 |
| 23 | 23 | 23 |
| 24 | 24 | 24 |
| 25 | 25 | 25 |
| 26 | 26 | 26 |
| 27 | 27 | 27 |
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| 29 | 29 | 29 |
| 30 | 30 | 30 |
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| 32 | 32 | 32 |
| 33 | 33 | 33 |
| 34 | 34 | 34 |
| 35 | 35 | 35 |
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| 38 | 38 | 38 |
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| 40 | 40 | 40 |
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| 42 | 42 | 42 |
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| 44 | 44 | 44 |
| 45 | 45 | 45 |
| 46 | 46 | 46 |
| 47 | 47 | 47 |
| 48 | 48 | 48 |
| 49 | 49 | 49 |
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| 51 | 51 | 51 |
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| 53 | 53 | 53 |
| 54 | 54 | 54 |
| 55 | 55 | 55 |
| 56 | 56 | 56 |
| 57 | 57 | 57 |
| 58 | 58 | 58 |
| 59 | 59 | 59 |
| 60 | 60 | 60 |
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| 62 | 62 | 62 |
| 63 | 63 | 63 |
| 64 | 64 | 64 |
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| 66 | 66 | 66 |
| 67 | 67 | 67 |
| 68 | 68 | 68 |
| 69 | 69 | 69 |
| 70 | 70 | 70 |
| 71 | 71 | 71 |
| 72 | 72 | 72 |
| 73 | 73 | 73 |
| 74 | 74 | 74 |
| 75 | 75 | 75 |
| 76 | 76 | 76 |
| 77 | 77 | 77 |
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| 79 | 79 | 79 |
| 80 | 80 | 80 |
| 81 | 81 | 81 |
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| 83 | 83 | 83 |
| 84 | 84 | 84 |
| 85 | 85 | 85 |
| 86 | 86 | 86 |
| 87 | 87 | 87 |
| 88 | 88 | 88 |
| 89 | 89 | 89 |
| 90 | 90 | 90 |
| 91 | 91 | 91 |
| 92 | 92 | 92 |
| 93 | 93 | 93 |
| 94 | 94 | 94 |
| 95 | 95 | 95 |
| 96 | 96 | 96 |
| 97 | 97 | 97 |
| 98 | 98 | 98 |
| 99 | 99 | 99 |
| 100 | 100 | 100 |

FT /note= "signal peptide"

FT /note= "N-myristoylation site"

FT /note= "N-glycosylation site"

FT /note= "N-myristoylation site"

FT /note= "N-glycosylation site"

FT /note= "N-glycosylation site"

FT /note= "N-myristoylation site"

FT /note= "N-myristoylation site"

FT /note= "N-glycosylation site"

/note="transmembrane protein"

/note= "N-myristoylation site"

```
/note= "N-myristoylation site"
```

```

EM      207  311
F1      /note= "N-myristoylation site"

```

| | | | |
|----|-------------------------------|-----|-----|
| EM | Modified site | 208 | 214 |
| F1 | /note= "N-glycosylation site" | | |

```

      Modificatio 263 360
      /note= "N-methylsilylation site"
      E1
      ET

```

| | | | | | |
|----|---------------|-----|-----|-------|----------------------|
| ET | Modified-site | 354 | 370 | /NO2= | N-nitrosylation site |
| E1 | | | | | |

N-methyl-*N*-propylcarbamoyl chloride
XX

XX EN 102000 / 1031-AE

| | |
|----|----|
| XX | 2 |
| XX | 4 |
| | 5 |
| | 6 |
| | 7 |
| | 8 |
| | 9 |
| | 10 |

| | |
|----|-----|
| XX | 1 |
| | 2 |
| | 3 |
| | 4 |
| | 5 |
| | 6 |
| | 7 |
| | 8 |
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| | 10 |
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PR 20-JUL-1999: 99US-0145070.

PR 17-AUG-1999; 99US-01493396.

PR 08-SEP-1999; 99WO-US20594.

PR 15-SEP-1999; 99WO-US21547.

PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 07-DEC-1999; 99US-0169495.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin LJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2001-050091/06.
DR N-PSDB; AAC87040.
XX
PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides -
XX
PS Claim 12; Fig 56; 244pp; English.
XX
CC The present sequence represents a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these
CC polypeptides are useful in the recombinant production of the
CC polypeptides, as a hybridisation probe to screen libraries to isolate
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene.
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPGPLVTNLRLFLFLGSLALAPPSRAQLQLHLPLANRLQAVEGGEVILPAWYTLHGEV 60

Db 1 mslpgplvtnlrlflflgslalapparaqlqlhlplanrlqaveggevllpawtytlhgev 60
QY 61 SSSQPEWEPFVWMEFKQKEKEDQVLSTYINGVTTSKPGVSLVYSMPSPNNLSLRLGLEQEKD 120
Db 61 sssqpewepfvwmefkqkekedqvlstyngvttskpgvslvyssmpsrnllslrlgleqekd 120
QY 121 SGPYSCSVNVODKQSGSRGHSIKTLEINLVLPAPPSCRLOGVPHVGANVTLSQSPRSK 180
Db 121 sgpyscsvnvodkqsgsrghsiktlelnlvlpappscrlgvyphvganvtlscqsprsk 180
QY 181 PAVQYQWDRQLPSFQTEFPALDIVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCNVTLE 240
Db 181 pavqyqwdrqlpsfqtffapaldivirgslstnlssmagvyvckahnevgtaqcnvtle 240
QY 241 VSTPGAAVAVAGAVGTGLVGLLAGLVLVYHRRGKALEEPANDIKDAIAPRTLPMPKS 300
Db 241 vstpgaaavavagavgtglvgllaglvlyhrrgkaleepandikedaiaprtlpmpks 300
QY 301 SPTISKNGTSSVTSARALRPHPGPRRGALTPTPSISOALPSRPLPTDGAHPQPISP 360
Db 301 sptiskngtssvtsaralrphpgpprgaltptplsalsgalpsrplptdgaahpqpiisp 360
QY 361 IPGGVSSSGLSRMGAVPVMPAQSOAGSLV 390
Db 361 ipgvsassglstrmgavpvmvpaqsagslv 390

RESULT 10

AAB80219
ID AAB80219 standard; Protein; 390 AA.
XX
AC AAB80219;
XX
DT 24-APR-2001 (first entry)
XX
DE Human PRO246 protein.
XX
KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.
XX
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US04414.
XX
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 05-JAN-2000; 99WO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Deansoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin LJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WT;
 XX
 DR WPI; 2001-081051/09.
 DR N-PSDB; AAF72379.
 XX
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
 PT Alzheimer's disease) -
 XX
 PS Claim 1; Fig 17; 393pp; English.
 XX
 CC The present sequence is one of sixty one novel secreted and
 CC transmembrane PRO polypeptides. The PRO polypeptides are
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
 CC endometrial bleeding angiogenesis, ischaemias such as coronary
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
 CC diabetes and retinal disorders such as retinitis pigmentosum.
 CC The PRO nucleic acids have applications in molecular biology, including
 CC use as hybridization probes, and in chromosome and gene mapping.
 XX
 SQ Sequence 390 AA:
 Query Match 100.0%; Score 2012; DB 22; Length 390;
 Best Local Similarity 100.0%; Pred. No. 5.8e-143;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
 0;
 QY 1 MISLPGPLVNTLRLFLGISALAPPSRAQQLHLPLNRQLQAVEGGEVLLPAMYTLHGEV 60
 Db 1 mislpgplvntlrlflgisalappstraqqlhlpntrlqaveggevllpawtclhgev 60
 QY 61 SSSQWEVFPVMWFRKQKEKDQVLSYINGVTTSKRCVSLVYSMPBRNLSRLREGLOEKD 120
 Db 61 sssqgewepfvmwffrkqekedqvlsyingvttskrcvslvysmpbrnlsrlreglqekd 120
 QY 121 SGPYSGSVNVODKQKSRGHSIKTIELNLVLPAPPSCRLOGVPHVGANVTLSGQSPRSK 180

Db 121 sgpyscsvnvodkqksgkrsghsktielelnlvppappscrilgvphvganvltscqgsprsk 180
 QY 181 PAVQYQWDRQLPSFQTFEPALADVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTL 240
 Db 181 pavqyqwdrrqlpsfqtfepaldvirgslsltnlssmagvyvckahnevgtacqncvtle 240
 QY 241 VSTGPGAAVAVGAVVGTLVGIGLAGIVLVYHRRGKALEEPANDIKEDALPRTLPMWPKS 300
 Db 241 vstgpgaaavavavvgtlvvgiglagivlvlyhrrgkaleepandikedalaprclpmwps 300
 QY 301 SDTISKNGTSSVTSARALRPHGPPRGALTPTPSLSSQALPSPRUPTDGAHPORISP 360
 Db 301 sdtiskngtssvtsaralrphgpprgaltptpslssqalpsprlptdgaahporisp 360
 QY 361 IPGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
 Db 361 ipgvsssglsrmgavpvmvpaqsgagslv 390
 RESULT 11
 AAB53082
 ID AAB53082 standard; Protein; 390 AA.
 XX
 AC AAB53082;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human angiogenesis-associated protein PRO246, SEQ ID NO:96.
 XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 PN WO200053753-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 05-JAN-2000; 2000WO-US00219.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.

PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Masters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2001-090793/10.
DR N-PSDB; AAC97441.
XX
XX
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -
XX
XX
XX Claim 69; Fig 38; 293pp; English.
XX
CC The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC angiogenic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or angiogenic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising
a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof.
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to
CC screen libraries to isolate cDNAs with sequence identity to PRO
proteins,
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
CC gene therapy. PRO nucleic acids can also be used to produce transgenic
CC animals useful for the development and screening of potential
CC therapeutic agents. The present sequence represents a PRO protein of the
invention.
XX
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;

Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
0;
QY 1 MISLPGPLVTNLLRFLFLGSLALAPPSRAQLHLHPANRLQAVEGGEVLPAMYTLHGEV 60
|||||
Db 1 mislpgplvtllrlflglalappsrdaqhlhpanrlaveggevlpawtytlhgev 60
QY 61 SSSQPEVFPFWMWFFKQKEKEDQVLSTINGTTSKRQVSLVYSMPSRNLSRLGLEQEKD 120
|||||
Db 61 sssqpevpfvmwffkqkexedqvlsyngvltckpjsvlsympsrlslrlglqekd 120
QY 121 SGPYSCSVNVODKQGRSGHSIKITELINVLVPPAPPCRLQGVPHVGANVTLSQSPRSK 180
|||||
Db 121 sgpyscsvnvdkqgrsgrhsikitlelnvlppappscrllgvpvhanvltscqpsrk 180
QY 181 PAVQYQWDRQLPSFQTFPAPALDIVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCWVTL 240
|||||
Db 181 pavqyqwdrlpsfqtffapaldvirgslsltnlssmagvyvckahnevgtacqnvtle 240
QY 241 VSTGPAAVAVAGAVGTLVGLAGLVLYHRRGKALEEPNANDIKEDALPRTLWPWKS 300
|||||
Db 241 vstgpaaavagavgtlvglaglvlyhrrgkaleepndikedalprtllwpwks 300
QY 301 SDTISKNGTSSVTSARALRPPHPPRGALTPTPSLSQALPSPRUPTTDGAHPQPISP 360
|||||
Db 301 sdtiskngtssvtsaralrpphpprgaltptpslsqalpsprlpttdgahpqpiisp 360
QY 361 IPGVSSSSGLSRMGAVPVMVPAQSQAGSLV 390
|||||
Db 361 ipgvsssglsrmgavpvmvpaqsgagslv 390

RESULT 12
AAE06610
ID AAE06610 standard; Protein; 390 AA.
XX
AC AAE06610;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein having hydrophobic domain, HP10801.
XX
KW Human, hydrophobic domain; gene therapy; nutritional supplement;
KW cell proliferation; immunomodulatory; autoimmune disorder;
antimicrobial;
KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
KW contraceptive; antiinfectility; antiinflammatory.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= Signal_peptide
FT Protein 31..390

FT /note= "Mature human protein with hydrophobic domain"
XX
PN WO200149728-A2.
PD 12-JUL-2001.
XX
PE 28-DEC-2000; 2000WO-JP09359.
XX
PR 06-JAN-2000; 2000JP-000585.
PR 06-JAN-2000; 2000JP-000588.
PR 11-JAN-2000; 2000JP-0002299.
PR 03-FEB-2000; 2000JP-0026862.
PR 03-MAR-2000; 2000JP-0058367.
XX
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.
XX
PI Kato S, Kimura T;
XX
DR WPI; 2001-418355/44.
DR N-PDB; AAD12605.
XX
PT Human proteins with hydrophobic domains and the nucleic acids encoding
PT them, useful for preventing diagnosing and treating e.g. cancer,
PT Alzheimer's and inflammation -
XX
PS Claim 1; Page 448-450; 563pp; English.
XX
CC The present sequence is human protein with hydrophobic domain,
CC HP10801. The polynucleotide and polypeptide of the invention
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The
CC polynucleotides
CC may be used to produce the polypeptide, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. The
CC polynucleotides and its complementary sequences may also be used as DNA
CC probes in diagnostic assays and also used in gene therapy. The
CC polypeptides may also be used as antigens in the production of
CC antibodies
CC and in assays to identify modulators of polypeptide expression and
CC activity. The polypeptides and nucleic acids may be used as nutritional
CC supplements, to modulate cytokine and cell proliferation activity, to
CC modulate immune stimulation or suppression (e.g. for the treatment of
CC microbial infections and autoimmune disorders such as multiple
CC sclerosis,
CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
CC haematopoiesis, to modulate tissue growth activity (e.g. for the
CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
CC disease), to modulate activin and inhibin activity (e.g. for controlling
CC fertility), to modulate chemotactic and chemokinetic activity, to
CC modulate haemostatic and thrombolytic activity, to modulate receptor
CC ligand activity, to modulate inflammation and to inhibit tumour growth.
XX
SQ Sequence 390 AA;

Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MISLPGELVNTILRLFLGLSALAPSPRAQIQHLHPANRLQAVEGSEVLPAMWYTLHGEV 60
DB 1 mislpgelvtlnllflfiglsalappraqqlhlpnrlqavegsevlpawylthgev 60
QY 61 SSSQPEWEPFVWMFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLLEGIOEKD 120
DB 61 sssqpewepfvwmffkqkexkedqvlsvyngvttskpgvslvyssmpsrnlslrllegioekd 120
QY 121 SGPYSCSVNVODKQKSRGHSIKTLELVLPAPAPSCRLQGVPHVGANVTLSQSPRSK 180
DB 121 sgpyscsvnvodkqksrghsiktlevlvpapapscrlqgvphganvltscgspbrsk 180
QY 181 PAVQYQWDRQLPSFQTFPAPALDIVRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE 240
DB 181 pavqyqwdrqlpstfqtffapaldivrgslsltnlssmagvyvckahnevgtaqcnvtle 240
QY 241 VSTGPGAAVAVGAVVGTVLVGLGLAGLVLYHRRGKALEEPANDIKEDAIAPRTLPMWPKS 300
DB 241 vstgpgaaavgavvgvtlvglglaglvlyhrrgkaleepandikedaiaprtlpwps 300
QY 301 SDTISKNGTLLSVTSARALRPHPGPRPGALTPTPSLSQALPSRLPTTDGAHPQFISP 360
DB 301 sdtiskngtlsvtsaralrpphpgprpgaltptpslsqalpsrlpttdgahpqfisp 360
QY 361 IPGVSSSSGLSRMGAVPVMVPAQSQAQSLV 390
DB 361 ipgvsssglsrmgavpvmvpaqsqagslv 390
RESULT 13
AAB90818
ID AAB90818 standard; Protein; 390 AA.
XX
AC AAB90818;
XX
DT 15-JUN-2001 (first entry)
XX
DE Human shear stress-response protein SEQ ID NO: 144.
XX
KW Human; shear stress-response protein; vascular disease;
KW arteriosclerosis.
XX
OS Homo sapiens.
XX
PN WO200125427-A1.
XX
PD 12-APR-2001.
XX
PE 02-OCT-2000; 2000WO-JP06840.
XX
PR 01-OCT-1999; 99JP-0280976.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJIT/) NOJIMA H.
XX

PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
XX
XX
DR WPI; 2001-266308/27.
DR N-PSDB; AAH02949.
XX
XX
PT DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis -
XX
XX
PS Claim 35; Page 599-601; 678pp; Japanese.
XX
XX
CC The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension.
XX
XX
SQ Sequence 390 AA;

Query Match 99.6%; Score 2004; DB 22; Length 390;
Best Local Similarity 99.7%; Pred. No. 2.3e-142;
Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps
0;

QY 1 MISLPGPLVTLRLRFLGLSALAPPSRAQIQHLHPANRLQAVEGGEVLLPAMYTLHGEV 60
|||||
Db 1 mislpgplvtnlrlflglalsalappsraqqlhpanrlqavegeevllpawylthgev 60
QY 61 SSSQPEWEPFVWMEFKQEKEDQVLSYINGVTTSKPGVSLVSMPSRNLSLRLEQLQEKD 120
|||||
Db 61 sssqpewepfvwmefkqekedqvlsyngvttskpgvslvsmprnlslrlleglqekd 120
QY 121 SGPYSCSVNVODKQGRSGHSIKTELINLVPPAPPSCRLOGVPHYGANVTLLSCQSPRSK 180
|||||
Db 121 sgpyscsvnvodkqgrsghsiktelnlvppappscriqgyphvganvtlscqsprsk 180
QY 181 PAVQYQMDRQLPSFQTFAPALDVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCNTLLE 240
|||||
Db 181 pavqyqwdrlpsfqtffapaldvirgslstnlssmagvyvckahnevgtacqnvtle 240
QY 241 VSTGPGAANVAGAVVGTLVGILGLVLLVYRRGKALEEPANDIKEDAIAPRTLBPWPKS 300
|||||
Db 241 vstgpgaavvagavvgtlvgilglvllvyrrgkaleepandikedaiaprtlpwps 300
QY 301 SDTISKNGTSSVTSARALRPHGPRRGALTPTPSLSSQALPSRPLPTPDGAHPQIPSP 360
|||||
Db 301 sdtiskngtssvtsaralrphgpprgaltptpslssqalpsrplptpdgahpqpisp 360
QY 361 IPGVSSSGLSRMGAVPVWVPAQSQAGSLV 390
|||||
Db 361 ipgvsssglsrmgavpvwvpaqsgagslv 390

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AAV76303;
23-MAR-2000 (first entry)
Fragment of human secreted protein encoded by gene 29.
Human; secreted protein; cancer; tumour; developmental abnormality;
foetal deficiency; blood disorder; immune system disorder; inflammation;
autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
therapy.
Homo sapiens.
WO9958660-A1.
18-NOV-1999.
06-MAY-1999; 99WO-US09847.
12-MAY-1998; 98US-0085093.
12-MAY-1998; 98US-0085094.
12-MAY-1998; 98US-0085105.
12-MAY-1998; 98US-0085180.
18-MAY-1998; 98US-0085906.
18-MAY-1998; 98US-0085920.
18-MAY-1998; 98US-0085921.
18-MAY-1998; 98US-0085922.
18-MAY-1998; 98US-0085923.
18-MAY-1998; 98US-0085924.
18-MAY-1998; 98US-0085928.
18-MAY-1998; 98US-0085925.
18-MAY-1998; 98US-0085927.
(HUMA-) HUMAN GENOME SCI INC.
Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;
Lafleur DW, Endress GA, Ebner R;
WPI; 2000-062296/05.
New isolated human genes and the secreted polypeptides they encode,
useful for diagnosis and treatment of e.g. cancers, neurological
disorders, immune diseases, inflammation or blood disorders -
Disclosure; Page 440-441; 475pp; English.
AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
AAV76124 to AAV76223 are the secreted proteins encoded by the 97 human
genes. This sequence represents a fragment of one of the human secreted
proteins. The genes and their corresponding secreted polypeptides are
useful for preventing, treating or ameliorating medical conditions,
e.g. by protein or gene therapy. Also pathological conditions can be
diagnosed by determining the amount of the new polypeptides in a sample

or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences shown in AAY76224 to AAY76424 represent fragments of the secreted proteins.

Sequence 389 AA;

Query Match 99.6%; Score 2003; DB 21; Length 389;
Best Local Similarity 99.7%; Pred. No. 2.7e-142;
Matches 388; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MISLPGPLVTLRLRFLGLSALAPPSRAQIQLHPANRLQAVEGGEVVLPAWYTLHGEV 60
1 mislpgplvtlnlrflglisalappraqqlhlpnrlqavegeevvlpaawytlhgev 60
61 SSSQPMVEVPFVWMFFKQKEKEDQVLSYINGVTTSPGVSLVYSMPSRNLSTRLGLEQEKD 120
61 sssqpmvevpfvmwffkqkakedqvlsyngvttspgvslyvsmpsrnlsrtrleglqekd 120
121 SGPYSCSVNVODKQKSRGHSIKITLELNVLVPPAPPSCRLOGVPHYGANVTLSQSPRSK 180
121 sgpyscsvnvodkqksrgshsikitlelnvlvpappscrlgvyphganvltscqsprsk 180
181 PAVQYOWDRQLPSFQTFAPALDIVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCNTVLE 240
181 pavqyowdrqlpsfqtfapaldivirgslstnlssmagvyvckahnevtaqcnavtle 240
241 VSTGPGAAVVAGAVVGTLVGILAGLVLYRRGKALEEPANDIKEDAIAPRTLPPWPKS 300
241 vstgpgaavvavagavvgtlvvgilaglvlyhrrgkaleepandikedaiaprtlpwpks 300
301 SDTISKNGTSSVTSARALRPHGPPRGALTPPSSLSQALPSPLPTTDGAHPQIPSP 360
301 sdtiskngtssvtसारalrphgpprgaltppsslsqalpsplpttdgaahpqipsp 360
361 IPGVSSSGLSRMGAVPVWVPAQSQAGSL 389
361 ipgvsssglsrmgavpvwvpaqsqagsl 389

RESULT 15
AAB65832
ID AAB65832 standard; Protein; 370 AA.

AC AAB65832;

DT 28-MAR-2001 (first entry)

XX

DE Human INTERCEPT 258 SEQ ID NO: 28.

Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder; developmental disorder; kidney disorder.

Homo sapiens.

WO200078808-A1.

28-DEC-2000.

19-JUN-2000; 2000WO-US16883.

18-JUN-1999; 99US-0336536.

(MILL-) MILLENNIUM PHARM INC.

Leiby KR, McKay C, Bossone S;

WPI; 2001-050109/06.

New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple sclerosis and asthma -

Claim 9; Page 228-229; 332pp; English.

The present invention provides the protein and coding sequences of the human and murine secreted or transmembrane proteins TANGO 253, TANGO 257, TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.

Sequence 370 AA;

Query Match 86.4%; Score 1738.5; DB 22; Length 370;
Best Local Similarity 94.2%; Pred. No. 1.8e-122;
Matches 341; Conservative 3; Mismatches 11; Indels 7; Gaps 1;

1 MISLPGPLVTLRLRFLGLSALAPPSRAQIQLHPANRLQAVEGGEVVLPAWYTLHGEV 60
1 mislpgplvtlnlrflglisalappraqqlhlpnrlqavegeevvlpaawytlhrev 60

61 SSSQPMVEVPFVWMFFKQKEKEDQVLSYINGVTTSPGVSLVYSMPSRNLSTRLGLEQEKD 120
61 sssqpmvevpfvmwffkqkakedqvlsyngvttspgvslyvsmpsrnlsrtrleglqekd 120

121 SGPYSCSVNVODKQKSRGHSIKITLELNVLVPPAPPSCRLOGVPHYGANVTLSQSPRSK 180
121 sgpyscsvnvodkqksrgshsikitlelnvlvpappscrlgvyphganvltscqsprsk 180

181 PAVQYOWDRQLPSFQTFAPALDIVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCNTVLE 240
181 pavqyowdrqlpsfqtfapaldivirgslstnlssmagvyvckahnevtaqcnavtle 240

OM protein - protein search, using sw model

Run on: August 19, 2002, 16:16:12 ; Search time 24.02 Seconds
(without alignments)

updates/sec 396.585 Million cell

Title: US-09-902-759-39

Perfect score: 2012

Sequence: 1 MSLPGLVTNLRFLFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/2/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | Query | Match | Length | DB | ID | Description |
|--------|-------|-------|-------|-------|-------------------|----|----|--------------------|
| 1 | 2012 | 100.0 | 390 | 2 | US-08-979-424-1 | | | Sequence 1, Appli |
| 2 | 353.5 | 17.6 | 365 | 4 | US-08-928-383B-26 | | | Sequence 26, Appli |
| 3 | 346 | 17.2 | 365 | 4 | US-08-928-383B-2 | | | Sequence 2, Appli |
| 4 | 345.5 | 17.2 | 365 | 4 | US-08-928-383B-23 | | | Sequence 23, Appli |
| 5 | 343 | 17.0 | 365 | 2 | US-08-979-424-3 | | | Sequence 3, Appli |
| 6 | 343 | 17.0 | 365 | 4 | US-09-272-496-2 | | | Sequence 2, Appli |
| 7 | 297 | 14.8 | 319 | 1 | US-08-597-495B-22 | | | Sequence 22, Appli |
| 8 | 297 | 14.8 | 319 | 4 | US-09-068-051A-22 | | | Sequence 22, Appli |
| 9 | 290.5 | 14.4 | 365 | 4 | US-08-928-383B-24 | | | Sequence 24, Appli |
| 10 | 289.5 | 14.4 | 387 | 4 | US-09-175-928-2 | | | Sequence 2, Appli |
| 11 | 258 | 12.8 | 318 | 4 | US-09-068-051A-32 | | | Sequence 32, Appli |

| | | | | | | | | |
|----|-------|-----|------|---|-------------------|--|--|--------------------|
| 12 | 176 | 8.7 | 299 | 4 | US-09-188-930-331 | | | Sequence 331, App |
| 13 | 176 | 8.7 | 299 | 4 | US-09-462-270-2 | | | Sequence 2, Appli |
| 14 | 171 | 8.5 | 299 | 4 | US-09-188-930-189 | | | Sequence 189, App |
| 15 | 158.5 | 7.9 | 501 | 2 | US-08-408-095-31 | | | Sequence 31, Appli |
| 16 | 153.5 | 7.6 | 344 | 2 | US-08-602-725-34 | | | Sequence 34, Appli |
| 17 | 152 | 7.6 | 1101 | 3 | US-08-986-485-2 | | | Sequence 2, Appli |
| 18 | 134 | 6.7 | 607 | 2 | US-08-752-307B-12 | | | Sequence 12, Appli |
| 19 | 133 | 6.6 | 321 | 6 | 5169835-17 | | | Patent No. 5169835 |
| 20 | 133 | 6.6 | 464 | 2 | US-08-602-725-32 | | | Sequence 32, Appli |
| 21 | 133 | 6.6 | 642 | 1 | US-08-217-299-1 | | | Sequence 1, Appli |
| 22 | 133 | 6.6 | 698 | 2 | US-08-602-725-36 | | | Sequence 36, Appli |
| 23 | 133 | 6.6 | 734 | 2 | US-08-389-459A-17 | | | Sequence 17, Appli |
| 24 | 133 | 6.6 | 734 | 3 | US-08-987-867A-17 | | | Sequence 17, Appli |
| 25 | 132.5 | 6.6 | 252 | 2 | US-08-414-657D-56 | | | Sequence 56, Appli |
| 26 | 132.5 | 6.6 | 287 | 2 | US-08-414-657D-48 | | | Sequence 48, Appli |
| 27 | 132.5 | 6.6 | 304 | 2 | US-08-414-657D-44 | | | Sequence 44, Appli |
| 28 | 132.5 | 6.6 | 308 | 2 | US-08-414-657D-46 | | | Sequence 46, Appli |
| 29 | 132.5 | 6.6 | 325 | 2 | US-08-414-657D-2 | | | Sequence 2, Appli |
| 30 | 132.5 | 6.6 | 325 | 2 | US-08-414-657D-41 | | | Sequence 41, Appli |
| 31 | 132.5 | 6.6 | 338 | 2 | US-08-414-657D-60 | | | Sequence 60, Appli |
| 32 | 132.5 | 6.6 | 1241 | 4 | US-09-040-774-2 | | | Sequence 2, Appli |
| 33 | 132 | 6.6 | 828 | 1 | US-08-261-304-2 | | | Sequence 2, Appli |
| 34 | 130 | 6.5 | 1091 | 3 | US-08-986-485-5 | | | Sequence 5, Appli |
| 35 | 129 | 6.4 | 917 | 1 | US-08-245-295-2 | | | Sequence 2, Appli |
| 36 | 129 | 6.4 | 917 | 1 | US-08-481-130-2 | | | Sequence 2, Appli |
| 37 | 129 | 6.4 | 917 | 1 | US-08-656-984A-2 | | | Sequence 2, Appli |
| 38 | 129 | 6.4 | 917 | 1 | US-08-485-604-2 | | | Sequence 2, Appli |
| 39 | 129 | 6.4 | 917 | 2 | US-08-487-595-2 | | | Sequence 2, Appli |
| 40 | 128.5 | 6.4 | 252 | 2 | US-08-414-657D-57 | | | Sequence 57, Appli |
| 41 | 128.5 | 6.4 | 287 | 2 | US-08-414-657D-49 | | | Sequence 49, Appli |
| 42 | 128.5 | 6.4 | 310 | 2 | US-08-414-657D-45 | | | Sequence 45, Appli |
| 43 | 128.5 | 6.4 | 315 | 2 | US-08-414-657D-47 | | | Sequence 47, Appli |
| 44 | 128.5 | 6.4 | 338 | 2 | US-08-414-657D-42 | | | Sequence 42, Appli |
| 45 | 128.5 | 6.4 | 338 | 2 | US-08-414-657D-43 | | | Sequence 43, Appli |

ALIGNMENTS

RESULT 1
US-08-979-424-1
; Sequence 1, Application US/08979424
; Patent No. 5942606
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,424
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0405 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGFET03
CLONE: 1232054
US-08-979-424-1

Query Match 100.0%; Score 2012; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 3.7e-168;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MISLPGPLVNLRLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVLPAMYTLHGEV 60
1 MISLPGPLVNLRLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVLPAMYTLHGEV 60
61 SSSQPEVFPVMWPFKQKEKEDQVLSYINGVTTSKPGVSLVYSMSRNLSLRLEGLQEKD 120
61 SSSQPEVFPVMWPFKQKEKEDQVLSYINGVTTSKPGVSLVYSMSRNLSLRLEGLQEKD 120
61 SSSQPEVFPVMWPFKQKEKEDQVLSYINGVTTSKPGVSLVYSMSRNLSLRLEGLQEKD 120
121 SGPYSCSVNVQDKGKSRGHSIKTLELNLVLPAPPPSCRLOGVPHVNAVTLSCQSPRSK 180
121 SGPYSCSVNVQDKGKSRGHSIKTLELNLVLPAPPPSCRLOGVPHVNAVTLSCQSPRSK 180
121 SGPYSCSVNVQDKGKSRGHSIKTLELNLVLPAPPPSCRLOGVPHVNAVTLSCQSPRSK 180
181 PAVOYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE 240
181 PAVOYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE 240
241 VSTGPGAAVAVGAVGTIVGLGLAGLVLLYHRRKALEBPANDIKEDATAIRTLPMWPKS 300
241 VSTGPGAAVAVGAVGTIVGLGLAGLVLLYHRRKALEBPANDIKEDATAIRTLPMWPKS 300
301 SDTISKNGTLSSVTSARALRPPHGPBRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPSP 360
301 SDTISKNGTLSSVTSARALRPPHGPBRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPSP 360

QY 361 IPGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
Db 361 IPGVSSSGLSRMGAVPVMVPAQSQAGSLV 390

RESULT 2
US-08-928-383B-26
Sequence 26, Application US/08928383B
Patent No. 6210921
GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
APPLICANT: and Marshall S. Horwitz
TITLE OF INVENTION: CAR, A No. 6210921e1 Cocksackievirus and Adenovirus
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: US/08/928,383B
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-383B-26

Query Match 17.6%; Score 353.5; DB 4; Length 365;
Best Local Similarity 27.8%; Pred. No. 4.7e-23;
Matches 113; Conservative 71; Mismatches 156; Indels 67; Gaps 15;

QY 9 VTNLRLFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVLPAMYTLHGEVSSQPEW 67
Db 1 MARLLCFVLLCGIADFT---SGLSITTPTEORIEKAKGETAVLPCKFTLSPE--DGGPLD 54

```

QY 68 VPFVWMPFKQKEKE--DQVUSYINGVTTSKPGVSLVY-----SMPSRNL 109
      : | : | | : | : |
Db 55 IE--WLISPSDNQIVDQVILLYSG-----DKIYDNYYPDLKGRVHFTSNDYKSGDA 103
      : | : | | : | : |
QY 110 SLRLEGLQEKDGPYSCSVNVQDKQKSRGHSIKTLELNVLPAPPPSCRLQGVPHVGAN 169
      : : | | | | | : | : | | | | : | : |
Db 104 SINVTNLQLSDIGTYQCKVK-----KAPGVANKKFLTLVLVKPSGTRCFYDGSSEIGND 157
      : : | | | | | : | : | | | | : | : |
QY 170 VTLSCOSPRKRPAYQYQWDRQLPSFQTFAPAL-DVIRGSLSTNLSSMAGVYVCAGHN 228
      : | : : | : | | | | : : : | | | : |
Db 158 FKIKCEPKEGSLPLQPEW-QKLSDSQTMPTPLAEMTSPVLSVKNASSEYSGTYSCCTVQN 216
      : | : : | : | | | | : : : | | | : |
QY 229 EVGTAQCNTVLE-VSTGPGAAGVAVGTLVGLLGLVLYHRR--GKALEEPAND 284
      : | : | : | : | : | | | | : | : : | | : |
Db 217 RVGSDQCMRLDVPVPPSNRAGTIAGAVIGTLALVLIGAILFCCHRRRREEKYEKEVHND 276
      : | : | : | : | : | | | | : | : : | | : |
QY 285 IKEDAIAPRTLPMPKSSDTISKNGTLLSVTSARALRPHGPPRPGALTPTPSSLSQLPS 344
      : | : | : | | | : : : | : : | : : | :
Db 277 IRED-----VPPPKSRTSTARSYIGSNHSSL-----GSMSPSNMEGYSKTOY 318
      : | : | : | | : : : | : : | : : | :
QY 345 PRLPTTDGAH-PQPLSPIPGCVSSGSLSRMGAVPVWVPAOSQAGSLV 390
      : : | : | : | : | : | | | | | : | : |
Db 319 NQVPSDFERAPQSPPLAPAKVAPNLSRMGAVPVMI PAOSKDGSLV 365
      : : | : | : | : | : | | | | | : | : |

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Search completed: August 19, 2002, 17:09:51
Job time: 3219 sec

OM protein - protein search, using sw model

Run on: August 19, 2002, 16:21:32 ; Search time 42.75 Seconds
(without alignments)

876.604 Million cell

updates/sec

Title: US-09-902-759-39

Perfect score: 2012

Sequence: 1 MSLPGLVLTNLLRFLFLGL.....SRMGAVPMVPAQSGSLV 390

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 176 | 8.7 | 299 | 2 | SS6749 |
| 2 | 162.5 | 8.1 | 344 | 2 | A27681 |
| 3 | 158.5 | 7.9 | 847 | 2 | JH0371 |
| 4 | 155.5 | 7.7 | 3707 | 2 | S18252 |
| 5 | 154.5 | 7.7 | 4391 | 2 | A38096 |
| 6 | 153.5 | 7.6 | 647 | 2 | A35648 |
| 7 | 153.5 | 7.6 | 1040 | 2 | A49356 |
| 8 | 152.5 | 7.6 | 521 | 2 | S34338 |
| 9 | 152 | 7.6 | 483 | 2 | T17346 |
| 10 | 151.5 | 7.5 | 1036 | 2 | S22383 |
| 11 | 151.5 | 7.5 | 4162 | 2 | T42633 |
| 12 | 150.5 | 7.5 | 521 | 2 | JC1508 |

13 150.5 7.5 1040 2 A34695 axonal glycoprotei
14 150 7.5 868 2 A46512 CD22 homolog/B lym
15 149.5 7.4 341 2 JC1512 biliary glycoprote
16 147 7.3 5175 2 T20992 hypothetical prote
17 147 7.3 5198 2 T43290 hemiscetin precurs
18 144 7.2 349 2 A34815 carcinoembryonic

a

19 143 7.1 862 2 I49583 differentiation an
20 142 7.1 278 2 A39037 carcinoembryonic

a

21 141.5 7.0 26926 1 I38344 titin, cardiac mus
22 141 7.0 458 2 JC1509 biliary glycoprote
23 139 6.9 458 1 WMM5R1 biliary glycoprote
24 138.5 6.9 495 2 A55181 pregnancy-specific
25 138.5 6.9 1323 2 P80568 connectin 3B - chi
26 138 6.9 278 2 JC1506 biliary glycoprote
27 138 6.9 419 2 B54312 pregnancy-specific
28 137 6.8 7962 2 I38346 elastic titin - hu
29 136.5 6.8 518 2 JC4024 poliovirus recepto
30 135.5 6.7 426 2 C55181 pregnancy-specific
31 135.5 6.7 426 2 B35334 pregnancy-specific
32 135 6.7 428 2 JS0032 pregnancy-specific
33 135 6.7 428 2 I57486 pregnancy-specific
34 134 6.7 240 2 JC4121 pregnancy-specific
35 134 6.7 436 2 B55181 pregnancy-specific
36 133 6.6 321 2 JH0395 biliary glycoprote
37 133 6.6 351 2 JH0396 biliary glycoprote
38 133 6.6 417 2 JH0394 biliary glycoprote
39 133 6.6 419 2 A36109 pregnancy-specific
40 133 6.6 464 2 C30127 transmembrane carc
41 133 6.6 526 1 A32164 biliary glycoprote
42 133 6.6 702 2 A36319 carcinoembryonic

a

43 132.5 6.6 166 2 A33402 pregnancy-specific
44 132.5 6.6 338 2 JC4776 limbic-system-asso
45 132.5 6.6 338 2 JC1238 opioid-binding pro

ALIGNMENTS

RESULT 1
S56749
Junctional adhesion molecule precursor - human
N,Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1;
platelet F11 receptor
C,Species: Homo sapiens (man)
C,Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C,Accession: A59406; S56749
R,Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.;
Iwamatsu, A.; Kita, T.
J. Immunol. 163, 553-557, 1999
A,Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes
redistribution of junctional adhesion molecule in human endothelial cells.
A,Reference number: A59406; MUID:99323940; PMID:10395639
A,Accession: A59406
A,Status: preliminary
A,Molecule type: DNA

OM protein - protein search, using SW model

Run on: August 19, 2002, 17:11:02 ; Search time 24.06 Seconds
(without alignments)

updates/sec 627.624 Million cell

Title: US-09-902-759-39
Perfect score: 2012
Sequence: 1 MSLPGLVTLNLRFLFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------------------|
| 1 | 353.5 | 17.6 | 365 | 1 | CXAR_MOUSE P97792 mus musculu |
| 2 | 343 | 17.0 | 365 | 1 | CXAR_HUMAN P78310 homo sapien |
| 3 | 297 | 14.8 | 319 | 1 | A33_HUMAN Q99795 homo sapien |
| 4 | 212 | 10.5 | 298 | 1 | JAM2_HUMAN P57087 homo sapien |
| 5 | 176 | 8.7 | 299 | 1 | JAM1_HUMAN Q97624 homo sapien |
| 6 | 168.5 | 8.4 | 300 | 1 | JAM1_MOUSE O88792 mus musculu |
| 7 | 167.5 | 8.3 | 298 | 1 | JAM1_BOVIN Q9xt56 bos taurus |
| 8 | 163 | 8.1 | 344 | 1 | CEA6_HUMAN P40199 homo sapien |
| 9 | 158.5 | 7.9 | 4393 | 1 | PGBM_HUMAN P98160 homo sapien |
| 10 | 155.5 | 7.7 | 3707 | 1 | PGBM_MOUSE Q05793 mus musculu |
| 11 | 153.5 | 7.6 | 847 | 1 | CD22_HUMAN P20273 homo sapien |
| 12 | 153.5 | 7.6 | 1040 | 1 | AXO1_HUMAN Q02246 homo sapien |
| 13 | 151.5 | 7.5 | 1036 | 1 | AXO1_CHICK P26865 gallus gall |
| 14 | 150.5 | 7.5 | 521 | 1 | CEA1_MOUSE P31809 mus musculu |
| 15 | 150.5 | 7.5 | 1040 | 1 | AXO1_RAT P22063 rattus norv |
| 16 | 146 | 7.3 | 515 | 1 | PVR1_PIG Q9g176 sus scrofa |
| 17 | 145 | 7.2 | 517 | 1 | PVR1_HUMAN Q15223 homo sapien |

| | | | | | |
|----|-------|-----|------|---|-------------------------------|
| 18 | 144 | 7.2 | 349 | 1 | CEA8_HUMAN P31997 homo sapien |
| 19 | 143 | 7.1 | 862 | 1 | CD22_MOUSE P35329 mus musculu |
| 20 | 142.5 | 7.1 | 1709 | 1 | SN_HUMAN Q9bzz2 homo sapien |
| 21 | 138.5 | 6.9 | 515 | 1 | PVR1_MOUSE Q9jxf6 mus musculu |
| 22 | 138 | 6.9 | 348 | 1 | KILO_RAT Q9z038 rattus norv |
| 23 | 138 | 6.9 | 419 | 1 | PSG4_HUMAN Q00888 homo sapien |
| 24 | 135.5 | 6.7 | 426 | 1 | PSGB_HUMAN Q00887 homo sapien |
| 25 | 135 | 6.7 | 428 | 1 | PSG3_HUMAN Q16557 homo sapien |
| 26 | 134.5 | 6.7 | 337 | 1 | G55A_CHICK Q98892 gallus gall |
| 27 | 133 | 6.6 | 526 | 1 | CEA1_HUMAN P13688 homo sapien |
| 28 | 133 | 6.6 | 702 | 1 | CEA5_HUMAN P06731 homo sapien |
| 29 | 132.5 | 6.6 | 338 | 1 | LAMP_HUMAN Q13449 homo sapien |
| 30 | 132.5 | 6.6 | 345 | 1 | OPCM_HUMAN Q14982 homo sapien |
| 31 | 132.5 | 6.6 | 345 | 1 | OPCM_RAT P32736 rattus norv |
| 32 | 132 | 6.6 | 252 | 1 | CEA3_HUMAN P40198 homo sapien |
| 33 | 131.5 | 6.5 | 349 | 1 | IACH_SCHAM Q26474 schistocerc |
| 34 | 131.5 | 6.5 | 538 | 1 | PVR2_HUMAN Q92692 homo sapien |
| 35 | 131 | 6.5 | 519 | 1 | ECTO_RAT P16573 rattus norv |
| 36 | 130.5 | 6.5 | 837 | 1 | NCM2_MOUSE Q35136 mus musculu |
| 37 | 130 | 6.5 | 761 | 1 | NCM2_HUMAN P13592 homo sapien |
| 38 | 130 | 6.5 | 917 | 1 | ICAS_MOUSE Q60625 mus musculu |
| 39 | 129.5 | 6.4 | 345 | 1 | OPCM_BOVIN P11834 bos taurus |
| 40 | 128.5 | 6.4 | 338 | 1 | LAMP_RAT Q62813 rattus norv |
| 41 | 128.5 | 6.4 | 837 | 1 | NCM2_HUMAN Q15394 homo sapien |
| 42 | 128 | 6.4 | 338 | 1 | LAMP_CHICK Q98919 gallus gall |
| 43 | 128 | 6.4 | 530 | 1 | PVR2_MOUSE P32507 mus musculu |
| 44 | 126.5 | 6.3 | 404 | 1 | RAGE_HUMAN Q15109 homo sapien |
| 45 | 126 | 6.3 | 335 | 1 | PSG5_HUMAN Q15238 homo sapien |

ALIGNMENTS

| RESULT | ID | CXAR_MOUSE | STANDARD; | PRT; | 365 AA. |
|--------|--|-----------------------------------|-----------|------|---------|
| AC | P97792; | 009052; | | | |
| DT | 30-MAY-2000 | (Rel. 39, Created) | | | |
| DT | 30-MAY-2000 | (Rel. 39, Last sequence update) | | | |
| DT | 01-MAR-2002 | (Rel. 41, Last annotation update) | | | |
| DE | Coxsackievirus and adenovirus receptor homolog precursor (mCAR). | | | | |
| GN | CXADR OR CAR. | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| OX | NCBI_TaxID=10090; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=liver; | | | | |
| RX | MEDLINE=97190109; PubMed=9036860; | | | | |
| RA | Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., | | | | |
| RA | Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.; | | | | |
| RT | "Isolation of a common receptor for Coxsackie B viruses and | | | | |
| RT | adenoviruses 2 and 5." | | | | |
| RL | Science 275:1320-1323(1997). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=C3H/MAI; | | | | |

OM protein - protein search, using sw model

Run on: August 19, 2002, 17:09:12 ; Search time 67.26 Seconds

(without alignments)

1003.093 Million cell

updates/sec

Title: US-09-902-759-39

Perfect score: 2012

Sequence: 1 MISTLPGBLVTNLRFLFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTREMBL_19:*
- 2: sp_archaea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mammal:*
- 8: sp_mhc:*
- 9: sp_organelle:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description

| | | | | | | |
|----|-------|-------|-----|----|--------|--------------------|
| 1 | 2012 | 100.0 | 390 | 4 | Q96AP7 | Q96ap7 homo sapien |
| 2 | 2009 | 99.9 | 390 | 4 | Q96RS0 | Q96t50 homo sapien |
| 3 | 1931 | 96.0 | 390 | 6 | Q95KI3 | Q95ki3 macaca faec |
| 4 | 1397 | 69.4 | 394 | 11 | Q925F2 | Q925f2 mus musculu |
| 5 | 641.5 | 31.9 | 204 | 11 | Q9D7I2 | Q9d7i2 mus musculu |
| 6 | 343 | 17.0 | 366 | 11 | Q9DBJ8 | Q9dbj8 mus musculu |
| 7 | 341.5 | 17.0 | 372 | 13 | Q90Y50 | Q90y50 brachydanio |
| 8 | 330 | 16.4 | 358 | 11 | Q9R066 | Q9r066 rattus norv |
| 9 | 324.5 | 16.1 | 327 | 4 | Q96IQ7 | Q96iq7 homo sapien |
| 10 | 320.5 | 15.9 | 325 | 4 | Q95791 | Q95791 homo sapien |
| 11 | 316 | 15.7 | 407 | 11 | Q9D2J4 | Q9d2j4 mus musculu |
| 12 | 307.5 | 15.3 | 373 | 4 | Q9H6B4 | Q9h6b4 homo sapien |
| 13 | 290 | 14.4 | 284 | 4 | Q9NX42 | Q9nx42 homo sapien |
| 14 | 287 | 14.3 | 373 | 11 | Q920S5 | Q920s5 mus musculu |
| 15 | 279.5 | 13.9 | 318 | 13 | Q91664 | Q91664 xenopus lae |
| 16 | 277.5 | 13.8 | 300 | 11 | Q9D9J0 | Q9d9j0 mus musculu |
| 17 | 276.5 | 13.7 | 300 | 11 | Q9DA22 | Q9da22 mus musculu |
| 18 | 272 | 13.5 | 352 | 11 | Q91W66 | Q91w66 mus musculu |
| 19 | 269 | 13.4 | 304 | 11 | Q9CVA4 | Q9cva4 mus musculu |
| 20 | 267.5 | 13.3 | 328 | 11 | Q9Z109 | Q9z109 mus musculu |
| 21 | 267.5 | 13.3 | 344 | 11 | Q9R067 | Q9r067 rattus norv |
| 22 | 266 | 13.2 | 335 | 13 | Q9PWR4 | Q9pwr4 gallus gall |
| 23 | 264.5 | 13.1 | 344 | 4 | Q9UKV4 | Q9ukv4 homo sapien |
| 24 | 263 | 13.1 | 335 | 13 | Q9YGH1 | Q9ygh1 gallus gall |
| 25 | 262.5 | 13.0 | 259 | 4 | Q95532 | Q95532 homo sapien |
| 26 | 259 | 12.9 | 319 | 11 | Q922D5 | Q922d5 mus musculu |
| 27 | 258 | 12.8 | 319 | 6 | Q9TU80 | Q9tu80 canis fami |
| 28 | 258 | 12.8 | 319 | 11 | Q9UKA5 | Q9jka5 mus musculu |
| 29 | 257 | 12.8 | 248 | 11 | Q9D0T4 | Q9d0t4 mus musculu |
| 30 | 256 | 12.7 | 319 | 6 | Q9TU79 | Q9tu79 sus scrofa |
| 31 | 253 | 12.6 | 335 | 13 | Q9YGV5 | Q9ygv5 gallus gall |
| 32 | 221 | 11.0 | 181 | 13 | Q91665 | Q91665 xenopus lae |
| 33 | 196 | 9.7 | 577 | 11 | Q9D221 | Q9d221 mus musculu |
| 34 | 186.5 | 9.3 | 977 | 4 | Q96RD9 | Q96rd9 homo sapien |
| 35 | 183 | 9.1 | 300 | 11 | Q9JHY1 | Q9jhy1 rattus norv |
| 36 | 176 | 8.7 | 298 | 11 | Q9YI59 | Q9ji59 mus musculu |
| 37 | 171 | 8.5 | 381 | 4 | Q9Y4A4 | Q9y4a4 homo sapien |
| 38 | 169.5 | 8.4 | 309 | 4 | Q96FL1 | Q96fl1 homo sapien |
| 39 | 169.5 | 8.4 | 310 | 4 | Q9BX67 | Q9bx67 homo sapien |
| 40 | 168.5 | 8.4 | 430 | 4 | Q15600 | Q15600 homo sapien |
| 41 | 166.5 | 8.3 | 310 | 11 | Q9D8B7 | Q9d8b7 mus musculu |
| 42 | 166 | 8.3 | 310 | 11 | Q9EPK4 | Q9epk4 mus musculu |
| 43 | 166 | 8.3 | 310 | 11 | Q9D1M9 | Q9dlm9 mus musculu |
| 44 | 164 | 8.2 | 538 | 4 | Q9NWQ7 | Q9nwg7 homo sapien |
| 45 | 163.5 | 8.1 | 512 | 4 | Q96DN8 | Q96dn8 homo sapien |

ALIGNMENTS

RESULT 1
Q96AP7
ID Q96AP7 PRELIMINARY; PRT; 390 AA.
AC Q96AP7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 41.2 KDA PROTEIN.

DE ENDOTHELIAL CELL-SELECTIVE ADHESION MOLECULE.
GN ESAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER/NIH;
RX MEDLINE=21238298; PubMed=11279107;
RA Hirata K.-I., Ishida T., Penta K., Rezaee M., Yang E., Wöhlgemuth J.,
RA Quèrtermous T.;
RT "Cloning of an immunoglobulin family adhesion molecule selectively
RT expressed by endothelial cells.";
RL J. Biol. Chem. 276:16223-16231(2001).
DR EMBL: AF361882; AAK51504.1; -.
SQ SEQUENCE 394 AA; 41810 MW; 3D2B354943A2227D CRC64;

Query Match 69.4%; Score 1397; DB 11; Length 394;
Best Local Similarity 72.3%; Pred. No. 1.1e-105;
Matches 285; Conservative 33; Mismatches 72; Indels 4; Gaps 3;

Qy 1 MISLPGDLVTLNLRLEFLGLSALAPPPSRAQLQHLHP--ANRLQAVEGGEVLLPAMYYTHG 58
|| | :||| ||||| || ||||:|:| | :|:|||| ||||| |:
Db 1 MILQAGTPETSLRLVFLGLSTLAAFSRAQMEHLHPGINKLLEAVEGGEVLLPAMYYMAR 60

Qy 59 EVSSSOPWEVFPVMWFFKQKEKE-DOLSYINGVTTSKPESVLVSMPBSNLSLRLEGIO 117
| | | | : : : : | | | | | | : : : : | | | | |
Db 61 EESWSHPREVILLIMPEOEKGEPNOVL SYINGVMTNKPGTALVHSISSRNVSLRGALO 120

Oy 118 EKDSGPCSVNVODKQKGSRGHSIKTLEINLVLPAPPSCRLOGVPHYGAMVTLLSCOSP 177
| | | | | : : | | | : : | | | | | : : | | | : :
Db 121 EGDSGYRCSTNVONDEGKSIGSHSISIEKLVLVPAPSPCSLGGVPYVGINTVTLNCKSP 180

Qy 178 RSKPAVOYOMDRLPSFQTFFAPALDIVIRGSLSTLNLSMAGVYVCANHEVGTAQCNU 237
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

Dp 181 RSKPTAOYOWERLAPSOSVEFGPALDAVRSLKLTNLSTAMSGYYVCKONRVEFAKCNY 240

Qy 238 TLEVSTGPGAAVVAGAVGTGLVLGLAGLVLVYHRKGALEBPANDIKEDAIAPRTLPW 297
|| : || ||||||| || | : ||||| || | ||| |||||||
Db 241 TLIDVMGSKAAVVAGAVGTGVGI V I AGI VLIVORRSKTLEFIANDIKEDAIAPRTLPW 300

QY 298 PKSSDTISKNGTLLSSVTSARALRPB-GPBRGALTPTPLSSLQAALPSRRLPTTDGAHQ 356
| | | | | | | | | | | : | | | | | | |
DB 301 TRGSDDTISKNGTLLSSVTSARALRPDAAVBPBGTFTPTPEVVSSOALSPLPRVDREPPQ 360

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Oy  357  EISPIPGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
      :| ||||| ||||| ||||| ||||| |||||
Db  361  AVSLTPGVSSALSRLMGAVPVMVPAQSQAGSLV 394

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RESULT 5

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|----|--------|--------------|------|-----|----|
| ID | Q9D7I2 | PRELIMINARY; | PRT; | 204 | AA |
|----|--------|--------------|------|-----|----|

DT 01-JUN-2001 (Tremblere1. 17, Created)

26

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Db      121  EGDSGTRCSTVNVQUNDEGKSIGHSIKSIETKVLVPPAPPSCSLQGVPPYVGTNVTLINCKSP 180
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Db      181  RSKPTAQYQWERLAP 195

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Search completed: August 19, 2002, 17:15:52
Job time: 400 sec

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:01:07 ; Search time 2294.29 Seconds
(without alignments)
updates/sec 16536.624 Million cell

Title: US-09-902-759-38
Perfect score: 1813
Sequence: 1 ggagccgcctgggtgtcag.....cataatgttctgtatgaataa 1813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
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9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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27: em_sts:*

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33: em_hcgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 1809.8 | 99.8 | 1838 | 9 | AF361746 Homo sapi |
| 3 | 1809 | 99.8 | 1821 | 6 | AX136161 Sequence |
| 4 | 1804.8 | 99.5 | 1816 | 6 | AX191598 Sequence |
| 5 | 1760.4 | 97.1 | 1831 | 6 | AX073678 Sequence |
| 6 | 1691.8 | 93.3 | 1734 | 9 | BC016868 Homo sapi |
| 7 | 1659.6 | 91.5 | 1855 | 9 | AB060855 Macaca fa |
| 8 | 1171.4 | 64.6 | 1173 | 6 | AX191588 Sequence |
| 9 | 861.6 | 47.5 | 1840 | 10 | AF361882 Mus muscu |
| 10 | 828.2 | 45.7 | 187960 | 9 | AP000866 Homo sapi |
| 11 | 793.2 | 43.8 | 101458 | 2 | AP000680 Homo sapi |
| 12 | 717.4 | 39.6 | 736 | 9 | AF2727292 Homo sapi |
| 13 | 531.2 | 29.3 | 637 | 6 | AX136493 Sequence |
| 14 | 453 | 25.0 | 541 | 6 | AX136640 Sequence |
| 15 | 441 | 24.3 | 441 | 6 | AX332845 Sequence |
| 16 | 339 | 18.7 | 221961 | 10 | AC073435 Mus muscu |
| 17 | 323.8 | 17.9 | 340 | 6 | AX331694 Sequence |
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| 29 | 70 | 3.9 | 611 | 9 | HSAB323034 Homo sapi |
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| 34 | 58 | 3.2 | 125020 | 9 | AF429315 Homo sapi |
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| 36 | 54.2 | 3.0 | 153292 | 2 | AP003635 Oryza sat |
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| 38 | 51 | 2.8 | 51 | 6 | AX161199 Sequence |
| 39 | 51 | 2.8 | 51 | 6 | AX161201 Sequence |
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| 41 | 50 | 2.8 | 50 | 6 | AX076928 Sequence |
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AX161200 Sequence
AX239602 Sequence
AX239607 Sequence

ALIGNMENTS

RESULT 1
AX076924
LOCUS AX076924 1813 bp DNA linear PAT
22-FEB-2001
DEFINITION Sequence 36 from Patent WO0105836.
ACCESSION AX076924
VERSION AX076924.1 GI:13121579
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1813)
AUTHORS Botstein,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A. and
Wood,W.I.
TITLE Polypeptidic compositions and methods for the treatment of tumors
JOURNAL Patent: WO 0105836-A 36 25-JAN-2001;
Genentech, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 368 a 559 c 484 g 402 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 cggcacctgcaggtccgtggtcccgcggtcggtcgccctgaactccgtccggcgagga 120
|||
Db 61 CGGCACTGCAAGTCCGTGCTGCCGCGGCTGGCGCTGACTCCGTCCCGCGCAGGA 120
QY 121 gggccatgattccctcccgggggccctgtgtgaccaaactgtgtgttctctcg 180
|||
Db 121 GGGCATGATTCCCTCCCGGGGCCCTGTGTGACCAACTGTGTGGTTTGTGTCTTG 180
QY 181 ggtcagtgccctcgccccccctcgggcgccagctgcaactgcaacttgccgccaacc 240
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QY 241 ggtcagtgccctcgccccccctcgggcgccagctgcaactgcaacttgccgccaacc 300
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LOCUS 07-MAY-2001

DEFINITION Homo sapiens endothelial cell-selective adhesion molecule (ESAM)

ACCESSION AF361746

VERSION AF361746.1 GI:13959017

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS Hirata,K.-I., Ishida,T., Penta,K., Rezaee,M., Yang,E., Wohlgemuth,J. and Quettermous,T.

TITLE Cloning of an Immunoglobulin Family Adhesion Molecule Selectively Expressed by Endothelial Cells

JOURNAL J. Biol. Chem. 276 (19), 16223-16231 (2001)

PUBMED 11279107

REFERENCE 2 (bases 1 to 1838)

AUTHORS Quettermous,T., Ishida,T. and Hirata,K.-I.

TITLE Direct Submission

JOURNAL Submitted (15-MAR-2001) Cardiovascular Medicine, Stanford University, 300 Pasteur Drive, Falk CVRC, Stanford, CA 94305-5406, USA

FEATURES

source location/qualifiers

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RESULT 3

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LOCUS AX136161 1821 bp DNA linear PAT
30-MAY-2001
DEFINITION Sequence 83 from Patent EP1067182.
ACCESSION AX136161
VERSION AX136161.1 GI:14272569
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1821)
Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
AUTHORS
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 83 10-JAN-2001;
Helix Research Institute (JP)
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AX191598 AX191598 1816 bp DNA linear PAT
15-AUG-2001
DEFINITION Sequence 120 from Patent WO0149728.
ACCESSION AX191598
VERSION AX191598.1 GI:15209789

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1816)
AUTHORS Kato, S. and Kimura, T.
TITLE Human proteins having hydrophobic domains and dnas encoding these proteins
JOURNAL Patent: WO 0149728-A 120 12-JUL-2001;
Proteogene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)
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06-FEB-2001
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ACCESSION AX073678
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1734)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA
 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxl.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

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 Cercopithecinae; Macaca.
 REFERENCE 1 (sites)
 AUTHORS Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
 Terano,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
 TITLE Isolation of full-length cDNA clones from macaque brain cDNA
 libraries
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1855)
 AUTHORS Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.

' TITLE Direct Submission
JOURNAL Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
(E - m a i l : k h a s h i @ n i h . g o . j p ,
URL: <http://www.nih.go.jp/yoiken/genebank/>,
Tel:81-3-5285-1111(ex.2120) , Fax:81-3-5285-1181)

COMMENT
Lab host: TOP10
Vector: PME18S-FL3 (Acc.No. AB09864)
R. Site1: DraIII (CACTGTGTG)
R. Site2: DraIII (CACCATGTG)
Description: 1st strand cDNA was primed with an oligo(dT) primer [ATGCGCCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of PME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert.

Libraries
were constructed by oligo-capping method (Sugano et al., , Institute of Medical Science, University of Tokyo).
Custom primer used for sequencing
(5' end primer [CTTCTGCTTAAAGTCGG];
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 AF361882
 LOCUS AF361882 1840 bp mRNA linear ROD
 08-MAY-2001
 DEFINITION Mus musculus endothelial cell-selective adhesion molecule (Esam)
 mRNA, complete cds.
 ACCESSION AF361882
 VERSION AF361882.1 GI:13991772
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Mus.
 REFERENCE 1 (bases 1 to 1840)
 AUTHORS Hirata,K.-I., Ishida,T., Penta,K., Rezaee,M., Yang,E.,
 Wohlgemuth,J. and Quertermous,T.
 TITLE Cloning of an immunoglobulin family adhesion molecule selectively
 expressed by endothelial cells
 JOURNAL J. Biol. Chem. 276 (19), 16223-16231 (2001)
 PUBMED 11279107
 REFERENCE 2 (bases 1 to 1840)
 AUTHORS Quertermous,T., Ishida,T. and Hirata,K.-I.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-2001) Cardiovascular Medicine, Stanford
 University, 300 Pasteur Drive, Falk CVRC, Stanford, CA
 94305-5406, USA
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 source location/Qualifiers
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 LV"
 BASE COUNT 404 a 498 c 482 g 456 t
 ORIGIN

| Query Match | 47.5%; | Score 861.6; | DB 10; | Length 1840; | Best Local Similarity 73.3%; | Pred. No. 1.9e-189; | Matches 1277; | Conservative 0; | Mismatches 424; | Indels 41; | Gaps 12; |
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| Qy 108 | ccccgccaaggagggcaatgatctccctcccggggccctggtgcaaccaactgtgcgg | 167 | Db 880 | GGAGCAGTTGGGGCACTTTGTTGGGTTGGTGTAGCTGGCGCTGCTGTGTAC | 939 | | | | | | |
| Db 100 | TCGGGCCAAGAGGGCCATATTCTTCAGGCTGGAAACCCCGAGACCAGCTTGTCGG | 159 | Qy 939 | caccgcccgggcaaggccctggagagaccgaatgatatacaagagagatgcattgct | 998 | | | | | | |
| Qy 168 | ttttgttcctggggtcgtgagtgccctcgccccctcgggggcccaagctgcaactgca | 227 | Db 940 | CAGCGCTGGAGCAAGCACTTGGAGAGCTGGCCATGATATCAAGAGATGCCATTGCT | 999 | | | | | | |
| Db 160 | GTTTGTTCCTGGGAGCTGAGTACCCTTGTGCTTCTCCGAGCTCAGATGAGTTGGAC | 219 | Qy 999 | ccccgaccctgcccctggcccagaagctcaagacaaactccaagaatggacccttcc | 1058 | | | | | | |
| Qy 228 | ttgcccgc-----caaccggttgcagcggttggaggagggaagtggtcttccagcg | 281 | Db 1000 | CCCCGACCTTGCTTGGACCAAGGCTCAGACAAATCTCAAGAAATGGACACTTCT | 1059 | | | | | | |
| Db 220 | GTGCCCCCGGCTCAACAATTTGAAGCGGTAGAGGAGAGAAAGATGTGTCCCGCC | 279 | Qy 1059 | tctgtcacctccgcacagagccctccggccacccca---tggccctcccaaggctgtgca | 1115 | | | | | | |
| Qy 282 | tggtacaccttgcacggggaggtgcttcaccccaagcattggagggtgccccttgtgatg | 341 | Db 1060 | TCGTTCACTCAGCAGCAGCTTTCGGGCCACCCAAAGCTGCTCTTCCAAAGCTGGCACA | 1119 | | | | | | |
| Db 280 | TGTTACACGATGGCACGGGAGAGTGTGTGCCACCCCGGAGGTGCCATCCTGATC | 339 | Qy 1116 | tgaaccccacagcccagctctctccagccaaggccctccctcaccaagactgccacgaca | 1175 | | | | | | |
| Qy 342 | tggtcttcaacacagaaagaagga--ggtacaggtgtgtcctacatcaatggggtc | 398 | Db 1120 | TTACTTCCACACCCAGTGTCTTACCCAGGCCCTGTCTCACAACAAGACTGCCAGGTA | 1179 | | | | | | |
| Db 340 | TGTTCTTGGACAAGAGGAGAGAACCAACCAAGGTGTTGTTTATTATATGAGTTC | 399 | Qy 1176 | gatggggcccaaccctcaaccaatatccccaatccctggtggggttctcctctgcttg | 1235 | | | | | | |
| Qy 399 | acaacaagcaaaccttgagatccttgytctactccatgcctcccggaaactgtccctg | 458 | Db 1180 | GATGAACCCCACTCAAGCAGCTGTCCCTGACCCCAAGTGGGGTTCTTCTGTGCTGTG | 1239 | | | | | | |
| Db 400 | ATGACAATAAATCTGGAAACAGCCCTGTGTCACTATCTTTCACGGAATGTGTCCCTG | 459 | Qy 1236 | agccgatgggtgtctgtcctgtgatggtgctgtgccagagtcgaagctgctctcgtga | 1295 | | | | | | |
| Qy 459 | cggctggaggtctccaaggagaagaactctggccctacagctgctccgtgaatgtgcaa | 518 | Db 1240 | AGCCGATGGGTGTGTGCTGTGATGTTGCTGCACAGAGTCAGGCTGGGTCTTGTGTG | 1299 | | | | | | |
| Db 460 | CGCTGGGGGCACTCCAGAGGAGACTCTGGGACTTACCGCTGTTCTGTCAATGTGTGAG | 519 | Qy 1296 | tgatgaccccaacactatgtgctaagaatcttggggtctccttccataaaggtcac | 1355 | | | | | | |
| Qy 519 | gacaaacaaggcaaatctaaggggccacagcatcaaaacttagaactcaatgtaactggtt | 578 | Db 1300 | TGATAGCCAGGCACTCATTTAGCTA---CATCTGTATCTGACTTTCTGTAAAGGTCTC | 1356 | | | | | | |
| Db 520 | AATGATGAAGGCMAAATATAGGCCACAGCACTCAAAAGCATAGAGCTCAAAATGTGCTT | 579 | Qy 1356 | c-tctagcacagagcctgagtcataggga-aagatcacactcctgaacccttagtactc | 1413 | | | | | | |
| Qy 579 | cctccagctcctccatcctgcgctcccaagggtgtgcccaatgtyggggcaaacgtgacc | 638 | Db 1357 | CTTTGGCAGACAGAGACTCAATCTTGGGAGGATGCCACATTTCTAGACTTCCAGTCTTT | 1416 | | | | | | |
| Db 580 | CCTCAGCTCCTCCATCTGTATGTTTACAGGGGTGTAACCTATGTGCGGACCATGTGACC | 639 | Qy 1414 | gccccacactcctcttactgtggaaaaacacactcagtaagaactaagttccaggagac | 1473 | | | | | | |
| Qy 639 | ctgagctgcagctctccaaggagtaagccgctgtccaataaccagtgggattcggcagctt | 698 | Db 1417 | GCTCTACTCTCTTCTATTTGTGAATTAATGGGCTCTCAGTAAGACTAAATCTGGGTCAA | 1476 | | | | | | |
| Db 640 | CTGAATGCAAGTCCCAAGAGATTAACCTACTGCTAGTACCAAGTGGAGAGGCTGGCC | 699 | Qy 1474 | agaaggagaagaagtgatctggaattggg-----aggagcctccaaccac | 1522 | | | | | | |
| Qy 699 | ccatcctccagacttctctgacacagcattagatgcatccgtgggtctttaagcttc | 758 | Db 1477 | AGGACAAAAGAGGAAATGGAAGCTGAGGTAGGGGGTTGGAGTAAGGAGGCTTCACCTTC | 1536 | | | | | | |
| Db 700 | CCATCTCCCAAGGTCTTCTTTGGACCAAGCCTTAGATGCTGTTGATCTTTAAAGCTTC | 759 | Qy 1523 | ccctgactcctcctt----atgaagcagctgcttaaatagctactcaccaagagtga | 1577 | | | | | | |
| Qy 759 | accaacttcgtctcccatggtctgagtcctatgtctgcaaggcccaacaatgagtgggc | 818 | Db 1537 | TCCCTGCTTCTCCCTGAAGCAGATGATGTGCGGAAGATCGGTAACCTCCAAAGGCT | 1596 | | | | | | |
| Db 760 | ACTAAGCTTTCATTGCGCATGTCTGAGTATGTCTGCAAGGCTCAAAAACGAGATGGGC | 819 | Qy 1578 | ggggcagagactccagtcactgagtcctccaaggccctctgactcttaaccaccctta | 1637 | | | | | | |
| Qy 819 | actgccaatgtaatgtgacgctggaagtgagcacaggccctggagctgcagtggtgct | 878 | Db 1597 | CTGAGGAGACTGCGCAGTCAATGA--TGCCCTGGCTGTGTATCTGTACACACACCTTA | 1654 | | | | | | |
| Db 820 | TTTGCAAGTCAACGTGACTTGGACGTGATGACAGGGTCCAAAGGCTGCAAGTGTGCT | 879 | Qy 1638 | tctaaccacaccccttggtccc-cactccagctccctgfatgatataactgctgagctg | 1696 | | | | | | |
| Qy 879 | ggagctggtgtgggtaccctggttggaactgggggttgctgctgggtgctcctctctgac | 938 | Db 1655 | TCTAATCTGTCTTTCGCTTGCCGTTGCTCATCTCCCTGTATTAATATTAACCTGTCTGCTG | 1714 | | | | | | |
| | | | Qy 1697 | gcttggttaggttttactggggca-gaggatagggaatctcctlatataaactaacatgaa | 1755 | | | | | | |
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DRAFT

SEQUENCE, 25 unordered pieces.

ACCESSION AP000680

VERSION AP000680.2 GI:8118868

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens DNA, clone:CMB9-25K9.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Homo sapiens 101,458 genomic DNA of 11q24

JOURNAL Published Only in Database (1999) In press

REFERENCE 2 (bases 1 to 101458)

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Direct Submission

JOURNAL Submitted (08-NOV-1999) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)

On May 31, 2000 this sequence version replaced gi:6997554.

----- Genome Center

Center: RIKEN Genomic Sciences Center (GSC)

Center code: RIKEN

Web site: http://hgp.gsc.riken.go.jp/

Contact: hattori@gsc.riken.go.jp/

----- Project Information

Center project name: HumDraft11

Center clone name: CMB9-25K9

----- Summary Statistics

Sequencing vector: PCR products; 100% of reads

Chemistry: Dye-terminator ET-amersham; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 89733 bases at least Q40

Consensus quality: 95050 bases at least Q30

Consensus quality: 97741 bases at least Q20

Insert size: 99058; sum-of-contigs

Quality coverage: 4.65x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists

25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished

sequence as soon as it is available and the accession number will be preserved

1 9364 contig of 9364 bp in length

9465 16830 contig of 7366 bp in length

16931 23631 contig of 6701 bp in length

23732 29864 contig of 6133 bp in length

29965 38284 contig of 5954 bp in length

38285 38384 contig of 100 bp

38385 44338 contig of 5954 bp in length

44339 44438 contig of 100 bp

44439 49484 contig of 5046 bp in length

49485 49584 contig of 100 bp

49585 55550 contig of 5966 bp in length

55551 55650 contig of 100 bp

55651 61139 contig of 5489 bp in length

61140 61239 contig of 100 bp

61240 65471 contig of 4232 bp in length

65472 65571 contig of 100 bp

65572 69042 contig of 3471 bp in length

69043 69142 contig of 100 bp

69143 73512 contig of 2534 bp in length

73513 73612 contig of 2799 bp in length

73613 76146 contig of 2933 bp in length

76147 76246 contig of 1405 bp in length

76247 79045 contig of 1458 bp in length

79046 79145 contig of 1237 bp in length

Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 25 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

1 9364: contig of 9364 bp in length

9365 9464: gap of 100 bp

9465 16830: contig of 7366 bp in length

16831 16930: gap of 100 bp

16931 23631: contig of 6701 bp in length

23632 23731: gap of 100 bp

23732 29864: contig of 6133 bp in length

29865 29964: gap of 100 bp

29965 38284: contig of 8320 bp in length

38285 38384: gap of 100 bp

38385 44338: contig of 5954 bp in length

44339 44438: gap of 100 bp

44439 49484: contig of 5046 bp in length

49485 49584: gap of 100 bp

49585 55550: contig of 5966 bp in length

55551 55650: gap of 100 bp

55651 61139: contig of 5489 bp in length

61140 61239: gap of 100 bp

61240 65471: contig of 4232 bp in length

65472 65571: gap of 100 bp

65572 69042: contig of 3471 bp in length

69043 69142: gap of 100 bp

69143 73512: contig of 4370 bp in length

73513 73612: gap of 100 bp

73613 76146: contig of 2534 bp in length

76147 76246: gap of 100 bp

76247 79045: contig of 2799 bp in length

79046 79145: gap of 100 bp

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RESULT 12
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03-AUG-2000
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ACCESSION AF277292
VERSION AF277292.1 GI:9664852
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 736)
AUTHORS Sim,D.L.C., Yeo,W.M. and Chow,V.T.K.
TITLE The novel human HUEL gene (C4orf1) encodes a protein that shares
homology with the DNA-binding domain of the XPA DNA repair
protein
and displays nuclear translocation in a cell cycle-dependent
manner
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 736)
AUTHORS Chow,V.T.K., Sim,D.L.C. and Yeo,W.M.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-2000) Microbiology, National University of
Singapore, 5, Science Drive 2, Singapore 117597, Singapore
FEATURES
source location/Qualifiers
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BASE COUNT 176 a 234 c 165 g 161 t
ORIGIN

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Best Local Similarity 99.9%; Pred. No. 5.3e-156;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1160 aagactgccacagacagatggggcccaacctcaaccaatatccccatccctggtggggct 1219
Db 121 AAGACTGCCACGACAGATGGGGCCCACTCAACCAATATCCCAATCCCTGTGGGGT 180
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Qy 1280 agctgctctctggtatgatgaccccaaccacatcatgtgctaaaggattggggctctcc 1339
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Db 421 AGTGTCCAGAGACAGAAAGAGAGAGAGATGGATCTGGAATTGGAGAGAGCCTCCACC 480
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 Db 661 TGGTATGTTTACTGTGGGCGACAGATAGGGAATCTTATTAATAACTAGTAATA 719

RESULT 13

AX136493 637 bp DNA linear PAT

30-MAY-2001 Sequence 415 from Patent EP1067182.

DEFINITION AX136493

ACCESSION AX136493

VERSION AX136493.1 GI:14272897

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 637)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: EP 1067182-A 415 10-JAN-2001; Helix Research Institute (JP)

FEATURES

source 1..637

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 116 a 202 c 185 g 129 t 5 others

ORIGIN

Query Match 29.3%; Score 531.2; DB 6; Length 637;
 Best Local Similarity 95.8%; Pred. No. 8.9e-113;
 Matches 576; Conservative 0; Mismatches 21; Indels 4; Gaps 3;

QY 1 99agccgcccctgggtgtcagcggctcggctccgcgcacagctccggcgctgcgcagcct 60
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 Db 12 GGAGCGCCCTGGGTGTACAGCGGCTGGCTCCGCCACAGCTCCGGCGTGCAGCCT 71

QY 61 cggcacctgcaggtccgtgcgtccgcggcgctgcggcccttgactccggtccggccagggga 120
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 Db 72 CGGCACTGACAGTCCGTGCGTCCCGCGCTGGCCCTGACTCCGTCGGCCAGGGA 131

QY 121 gggccatgattccctccggggccctctgtgaccaactgtcgggttttctctcgtg 180
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 Db 132 GGGCCATGATTTCTTCCTCCGGGGCCCTGTGACCACTTGCTGGGTTTGTCTCG 191

QY 181 ggcctgagtcctcgcgcgcgcctcgcgcggccagctgcaactgcaactgcccgcgaacc 240
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 Db 192 GGCTGAGTGCCCTCGCGCCCTCGCGGGCCAGCTGCACTGCACTTGCCCGCAACC 251

QY 241 ggttcagggcgggtgagggaggggaagtgtgtctccagcgtggtacacctgcagggg 300
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 Db 252 GGTTCAGGCGGGTGAAGGAGGGGAATGTGTCTTCAGCGGTGTACACCTTGACGAGG 311

QY 301 aggtgttcacatccacgcatggaggtgcctctgtgatgtgtgtcttcaacagaag 360
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 Db 312 AGGTGTCTTCATCCACGACCATGGAGGTGCCCTTGTGATGTGTCTTCAACAGAAAG 371

QY 361 aaaagagatcaggtgtgttctcatcatatgggttcacaacagaacacttgagrat 420
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 Db 372 AAAAGAGATCAGTGTGTCTTACATCATATGGGGTCAACAACGAACCTTGAGTAT 431

QY 421 ccttgtctactccatgccctccgcgaacctgtccctgcgctgagaggtctccaggaga 480
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 Db 432 CCTGTCTACTCCATGCCCCCTCCGGAACCTGTCCGTGGCTGAGAGGTCTCCAGGAG 491

QY 481 aagactctggccctcactcagctgtccg-tgaatgtgcaagacaac-aagcaatctag 538
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 Db 492 AAAGACTCTGGCCCTACAGCTGCTCCGTGAATGTGCACAACAAAGCAATCTTA 551

QY 539 gggccaca-gcatcaaaccttagaactcaatgtactgtgtcctccagctcccatcc 596
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 Db 552 GGCCACAGCATCAAAAACCTTANAACTCAATGTACTGTCTCCANCTNTCCATCC 611

QY 597 t 597
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 Db 612 T 612

RESULT 14

AX136640/c 541 bp DNA linear PAT

LOCUS AX136640

30-MAY-2001

DEFINITION Sequence 562 from Patent EP1067182.

ACCESSION AX136640

VERSION AX136640.1 GI:14273044

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 541)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.

TITLE Secretory protein or membrane protein

JOURNAL Patent: EP 1067182-A 562 10-JAN-2001; Helix Research Institute (JP)

FEATURES

source 1..541

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 153 a 120 c 110 g 141 t 17 others

ORIGIN

Query Match 25.0%; Score 453; DB 6; Length 541;
 Best Local Similarity 91.8%; Pred. No. 1.3e-94;
 Matches 490; Conservative 0; Mismatches 42; Indels 2; Gaps

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:04:12 ; Search time 220.41 Seconds
(without alignments)
14122.616 Million cell updates/sec

Title: US-09-902-759-38

Perfect score: 1813

Sequence: 1 ggaagccgcctcggtgtcag.....catacgtttgtatgaaaaa 1813

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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| 2 | 1813 | 100.0 | 1813 | 20 | AAK28436 | EGF-like homologue |
| 3 | 1813 | 100.0 | 1813 | 21 | AAK30052 | Human PRO246 nucle |
| 4 | 1813 | 100.0 | 1813 | 22 | AAK21412 | Human cDNA sequenc |
| 5 | 1813 | 100.0 | 1813 | 22 | AAK60372 | PRO246 coding sequ |
| 6 | 1813 | 100.0 | 1813 | 22 | AAK87040 | Nucleotide sequenc |
| 7 | 1813 | 100.0 | 1813 | 22 | AAK72379 | Human PRO246 cDNA. |
| 8 | 1813 | 100.0 | 1813 | 22 | AAK97441 | Human angiogenesis |
| 9 | 1809 | 99.8 | 1821 | 22 | AAK93785 | Human cDNA encodin |
| 10 | 1806.6 | 99.6 | 1827 | 22 | AAK02949 | Human shear stress |
| 11 | 1804.8 | 99.5 | 1816 | 22 | AAK12605 | Human protein havi |
| 12 | 1802 | 99.4 | 1954 | 21 | AAK23441 | CDNA encoding huma |
| 13 | 1783.8 | 98.4 | 1932 | 21 | AAK265278 | Human secreted pro |
| 14 | 1760.4 | 97.1 | 1831 | 22 | AAK85076 | Atherosclerosis-as |
| 15 | 1757.6 | 96.9 | 1869 | 22 | AAK44978 | Human INTERCEPT |
| 16 | 1756 | 96.9 | 1869 | 22 | AAK45014 | Human secreted pro |
| 17 | 1756 | 96.9 | 1869 | 22 | AAK45015 | Human secreted pro |
| 18 | 1756 | 96.9 | 1869 | 22 | AAK45016 | Human secreted pro |
| 19 | 1756 | 96.9 | 1869 | 22 | AAK45017 | Human secreted pro |
| 20 | 1440.8 | 79.5 | 1748 | 22 | ABA09181 | Human viral recept |
| 21 | 1440.8 | 79.5 | 1748 | 22 | AAK59707 | Human polynucleoti |
| 22 | 1376 | 75.9 | 1387 | 20 | AAK87000 | Human viral recept |
| 23 | 1083.2 | 59.7 | 1290 | 20 | AAK200447 | Human secreted pro |
| 24 | 1069.8 | 59.0 | 1110 | 22 | AAK44979 | Human INTERCEPT |
| 25 | 1066.2 | 58.9 | 1110 | 22 | AAK45046 | Human secreted pro |
| 26 | 1068.2 | 58.9 | 1110 | 22 | AAK45047 | Human secreted pro |
| 27 | 1068.2 | 58.9 | 1110 | 22 | AAK45048 | Human secreted pro |
| 28 | 1068.2 | 58.9 | 1110 | 22 | AAK45049 | Human secreted pro |
| 29 | 1010.4 | 55.7 | 1606 | 22 | AAK57921 | Human polynucleoti |
| 30 | 863.2 | 47.6 | 1846 | 22 | AAK45020 | Murine secreted pr |
| 31 | 861.6 | 47.5 | 1846 | 22 | AAK44981 | Murine INTERCEPT |
| 32 | 861.6 | 47.5 | 1846 | 22 | AAK45018 | Murine secreted pr |
| 33 | 861.6 | 47.5 | 1846 | 22 | AAK45021 | Murine secreted pr |
| 34 | 860 | 47.4 | 1846 | 22 | AAK45019 | Murine secreted pr |
| 35 | 730.2 | 40.3 | 1182 | 22 | AAK45052 | Murine secreted pr |
| 36 | 728.6 | 40.2 | 1182 | 22 | AAK44982 | Murine INTERCEPT |
| 37 | 728.6 | 40.2 | 1182 | 22 | AAK45050 | Murine secreted pr |
| 38 | 728.6 | 40.2 | 1182 | 22 | AAK45053 | Murine secreted pr |
| 39 | 727 | 40.1 | 1182 | 22 | AAK45051 | Murine secreted pr |
| 40 | 578.4 | 31.9 | 1288 | 22 | AAK10122 | Mouse 10.3 kDa pro |
| 41 | 531.2 | 29.3 | 637 | 22 | AAK93981 | Primer specific fo |
| 42 | 453 | 25.0 | 541 | 22 | AAK94128 | Primer specific fo |
| 43 | 251.2 | 14.2 | 571 | 22 | AAK97944 | Murine 7-transmemb |
| 44 | 226.4 | 12.5 | 564 | 22 | AAK97943 | Murine 7-transmemb |
| 45 | 208 | 11.5 | 533 | 22 | AAK97945 | Murine 7-transmemb |

ALIGNMENTS

RESULT 1
AAK52221
ID AAK52221 standard; DNA; 1813 BP.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

XX AAX52221;
AC
XX
DT 25-JUN-1999 (first entry)
XX
DE Protein PRO246 cDNA clone DNA35639-1172.
XX
KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
KW fibromodulin; dermal scarring; Usher Syndrome; Atrophla areata;
KW anti-thrombotic; wound healing; tissue repair; ss.
XX
OS Homo sapiens.
XX
PN W09914328-A2.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-US19330.
XX
PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059113.
PR 17-SEP-1997; 97US-0059115.
PR 17-SEP-1997; 97US-0059117.
PR 17-SEP-1997; 97US-0059119.
PR 17-SEP-1997; 97US-0059121.
PR 17-SEP-1997; 97US-0059122.
PR 17-SEP-1997; 97US-0059124.
PR 18-SEP-1997; 97US-0059263.
PR 18-SEP-1997; 97US-0059266.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 21-OCT-1997; 97US-0063486.
PR 24-OCT-1997; 97US-0062814.
PR 24-OCT-1997; 97US-0062816.
PR 24-OCT-1997; 97US-0063045.
PR 24-OCT-1997; 97US-0063120.
PR 24-OCT-1997; 97US-0063121.
PR 24-OCT-1997; 97US-0063127.
PR 24-OCT-1997; 97US-0063128.
PR 27-OCT-1997; 97US-0063329.
PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063541.
PR 28-OCT-1997; 97US-0063542.
PR 28-OCT-1997; 97US-0063544.
PR 28-OCT-1997; 97US-0063549.
PR 28-OCT-1997; 97US-0063550.
PR 28-OCT-1997; 97US-0063564.
PR 29-OCT-1997; 97US-0063435.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063738.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.

PR 29-OCT-1997; 97US-0063735.
PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.
XX
XX (GETH) GENENTECH INC.
XX
XX
PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
XX
XX WPI; 1999-229533/19.
DR P-PSDB; AAY13351.
DR
XX
PT New isolated human genes and polypeptides used in, e.g. treatment of
PT Gastrointestinal ulceration
XX
XX
PS Claim 2; Fig 16; 320pp; English.
XX
CC AAX52213-74 encode secreted and transmembrane human proteins, and are
CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
CC fetal brain, fetal liver and fetal retina. The encoded polypeptides
CC have specific uses based on their homology to known polypeptides,
CC e.g. PRO211 and PRO217 can be used for disorders associated with the
CC preservation and maintenance of gastrointestinal mucosa and the repair
CC of acute and chronic mucosal lesions (e.g. enterocolitis,
CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
CC microvillus atrophy), skin diseases associated with abnormal
CC keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as
CC lung squamous cell carcinoma of the vulva and gliomas), potent effects
on
CC cell growth and development, diseases related to growth or survival of
CC nerve cells including Parkinson's disease, Alzheimer's disease, ALS,
CC neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for
CC reducing dermal scarring. PRO264 can be used as a target for anti-tumor
CC drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophla
CC areata; PRO269 can be used as an anti-thrombotic agent; PRO287
CC polypeptides and portions may have therapeutic applications in wound
CC healing and tissue repair; PRO317 can be used for treating problems of
CC the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.
in the heart of genital tract.
XX
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 20; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

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Db 1741 taaactaacatgaatatgtgttcttccatttgcacaattcaataaagatacataatg 1800
Qy 1801 ttctgatgaaaaa 1813
|||||
Db 1801 ttctgatgaaaaa 1813
RESULT 2
AAx28436
ID AAx28436 standard; DNA; 1813 BP.
XX
AC AAx28436;
XX
DT 22-JUN-1999 (first entry)
XX
DE EGF-like homologue PRO246 coding sequence.
XX
KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261;
PRO246;
KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;
KW FGF-8 homologue; ss.
XX
OS Homo sapiens.
XX
PN WO914327-A2.
XX
PD 25-MAR-1999.
XX
PF 10-SEP-1998; 98WO-US18824.
XX
PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059114.
PR 17-SEP-1997; 97US-0059117.
PR 18-SEP-1997; 97US-0059263.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062285.
PR 24-OCT-1997; 97US-0062816.
PR 29-OCT-1997; 97US-0063704.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;
PI Roy M, Wood WI;
XX
XX WPI; 1999-229532/19.
DR P-PSDB; AAY05286.
XX
XX
PT Antibodies against specific proteins overexpressed in tumours
XX
PS Example 1; Fig 27; 130pp; English.
XX
CC This sequence encodes the EGF-like homologue PRO246.
CC The invention relates to antibodies (Ab) that bind to any of the
CC polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211;
CC PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit

CC expression and/or activity of (I) are used: (i) to inhibit growth of
CC tumours; and (ii) as diagnostic/prognostic reagents for detection or
CC quantification of (I) in cells or tissues, by standard immunoassays,
with
CC overexpression being indicative of cancer. For therapeutic use, the Ab
CC may be conjugated to a toxin, chemotherapeutic agent or radioisotope.
CC Genes expressing (I), many of which are growth factor homologues, are
CC overexpressed in some cases of cancer.

XX
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 20; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

Qy 1 ggaagccgcctgggtgtgcagcggctcggtcccgccagcgtcccgccgtcgagcct 60
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Db 1 ggaagccgcctgggtgtgcagcggctcggtcccgccagcgtcccgccgtcgagcct 60
Qy 61 cggcacctgcagagtcggtcggtcccgccggtcggtcgccctgactccgtccggccaagg 120
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Db 121 gggccatgatccctcccggggccccctggtgaccaaactgtcggttttgttctcg 180
Qy 181 ggtgagtgccctcgcccccctcgccggccagctgcaactgtgcccgaacc 240
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Qy 1501 attggagaggagcctccaccaccctgactcctccttatgaagccagctgctgaaattag 1560
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Qy 1561 ctactcaccaagagtgaaggggcagagacttccagctcagtgaagctcccaagccccctga 1620
Dh 1561 ctactcaccaagagtgaaggggcagagacttccagctcagtgaagctcccaagccccctga 1620
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Dh 1621 tctgtacccccaccctcttaacaccacccttggctcccactccagctccctgtatgat 1680
Qy 1681 ataacctgtcaggtcgtgcttgagtttaactgaggggcagagataggaaatctctat 1740
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Qy 1741 taaactaacatgaatatgtgttcttcattgtcaaatttaataaagatacataatg 1800
Dh 1741 taaactaacatgaatatgtgttcttcattgtcaaatttaataaagatacataatg 1800
Qy 1801 ttgtatgaaaaa 1813
Dh 1801 ttgtatgaaaaa 1813

RESULT 3
AAA30052
ID AAA30052 standard; cDNA; 1813 BP.

XX AC AAA30052;
XX DT 09-AUG-2000 (first entry)
XX DE Human PRO246 nucleotide sequence.

XX KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261;
PRO246;
KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;
KW cell growth; proliferation; cell surface virus receptor; ADEPT;
KW antibody dependent enzyme mediated prodnrg therapy; ss.

OS Homo sapiens.

XX PN W0200015666-A2.

XX PD 23-MAR-2000.

XX PF 08-SEP-1999; 99WO-US20594.

XX PR 10-SEP-1998; 98US-0099803.

XX PR 10-SEP-1998; 98WO-US18824.

XX PA (GETH) GEMENTECH INC.

XX PI Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;

XX WPI; 2000-271386/23.

XX DR P-PSDB; AAY88574.

XX New isolated antibodies which bind to specific polypeptides used for
 PR diagnosis and treatment of neoplastic cell growth and proliferation -
 XX
 PS Example 8; Fig 15; 200pp; English.
 XX
 CC This sequence represents a human PRO246 nucleotide sequence. PRO246 is
 CC probably a cell surface virus receptor. The invention relates to
 CC isolated
 CC antibodies which bind to a polypeptide. The "PRO" polypeptides are
 CC encoded by genes which are over expressed in the genome of tumour cells.
 CC Vectors and host cells comprising the nucleic acid encoding the
 CC antibodies are used in the production of the antibodies. The antibodies
 CC and nucleic acids encoding them are used for diagnosing a tumour in a
 CC mammal. The antibodies are used for inhibiting the growth of tumour
 CC cells
 CC and identifying compounds that inhibit a biological or immunological
 CC activity of and/or expression of a PRO187, PRO533, PRO214, PRO240,
 CC PRO211, PRO230, PRO261, PRO246 or PRO317 polypeptide. The antibody can
 CC be
 CC used in antibody dependent enzyme mediated prodrug therapy (ADEPT) by
 CC conjugating the antibody to a prodrug-activating enzyme which converts
 CC a
 CC prodrug to an anti-cancer drug. The antibodies can be fluorescently
 CC labelled and monitored by light microscopy, flow cytometry or
 CC fluorimetry
 CC for diagnosis and prognosis of tumours.
 CC
 XX
 SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 21; Length 1813;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagccgcccgtgggtgtcagcggctcggtcccgcgacgctccggccgtcgcagcct 60
 Db |
 QY 1 ggagccgcccgtgggtgtcagcggctcggtcccgcgacgctccggccgtcgcagcct 60
 Db |
 QY 61 cggcacctcgaggtccgtgcgtcccgcgctggcgccctgaactccgtcccgccaggga 120
 Db |
 QY 61 cggcacctcgaggtccgtgcgtcccgcgctggcgccctgaactccgtcccgccaggga 120
 Db |
 QY 121 gggccatgattccctccgggggccccctgtgtgaccaactgtgcggttttctgtcctgg 180
 Db |
 QY 121 gggccatgattccctccgggggccccctgtgtgaccaactgtgcggttttctgtcctgg 180
 Db |
 QY 181 ggtcgaagtgccttcggcgccccctcgggggccacgtgcaactgtgacattgcccggcaacc 240
 Db |
 QY 181 ggtcgaagtgccttcggcgccccctcgggggccacgtgcaactgtgacattgcccggcaacc 240
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 QY 241 ggttcagagcggtggaagggaagggaagtgtgtcttcagcgtgtgtacacctgtgacgggg 300
 Db |
 QY 241 ggttcagagcggtggaagggaagggaagtgtgtcttcagcgtgtgtacacctgtgacgggg 300
 Db |
 QY 301 aggtgtcttcattccagcgaatgggaaggtgccttctgtatgtgttctcaacagagaag 360
 Db |

Db 301 aggtgtcttcattccagcgaatgggaaggtgccttctgtatgtgttctcaacagagaag 360
 QY 361 aaaggaggaatcaggtgtgtgtctctacatcaatggggtcacaaagaacactggaat 420
 Db |
 QY 361 aaaggaggaatcaggtgtgtgtctctacatcaatggggtcacaaagaacactggaat 420
 Db |
 QY 421 ccttgttactccatcgccctcccggaacactgtccctgcggtgtgagggttccaggaga 480
 Db |
 QY 421 ccttgttactccatcgccctcccggaacactgtccctgcggtgtgagggttccaggaga 480
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 QY 481 aagacttggccccctacagctgtccgtgaatgtgcaagacaacaaggcaactgaagg 540
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 QY 541 gccacagcatcaaaacttagaactcaatgtactgtgtccctccagctccctcatctgcgc 600
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 QY 601 gtctccagggtgtgcccccatgtgggggcaaacgtgacccctgagctgccaagtccaagga 660
 Db |
 QY 601 gtctccagggtgtgcccccatgtgggggcaaacgtgacccctgagctgccaagtccaagga 660
 Db |
 QY 661 gtaagcccgctgtccaataccagtgagtcggcagcttccactccctccagacttcttg 720
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 Db |
 QY 721 caccagcatatgattgtcatccgtgggtctttaaagccctcaccaaccttgcgttccatgg 780
 Db |
 QY 721 caccagcatatgattgtcatccgtgggtctttaaagccctcaccaaccttgcgttccatgg 780
 Db |
 QY 781 ctggagtcatagtctgcaaggcccaaatgagtgggcactgcccgaatgtaatgtgacgc 840
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 Db |
 QY 841 tggaaagtgaacacagggcctggagctgcagtggtgtgtcggagctgtgtggttaccctgg 900
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 QY 841 tggaaagtgaacacagggcctggagctgcagtggtgtgtcggagctgtgtggttaccctgg 900
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 QY 901 ttggaactggggttgcgtggctgggtgtccctctgtaccaccgcgggggcaaggccctgg 960
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 QY 961 aggaagccagcaatgatatacaaggagagatgcattgtcccccgaacccctgcctggcca 1020
 Db |
 QY 961 aggaagccagcaatgatatacaaggagagatgcattgtcccccgaacccctgcctggcca 1020
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 QY 1141 gccaggccctgcctccaccaagactgccaacagatgggagccacccctcaaccaatat 1200
 Db |

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 |||
 Db 1201 ccccatcctcgtgggttcttcctcctcgtcgtcgaagccgcatgggtcgtcgtga 1260
 |||
 QY 1261 tgggtcctgcagagatcaagctgcctcctgtatgatgaccccatcatcggcta 1320
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 Db 1261 tgggtcctgcagagatcaagctgcctcctgtatgatgaccccatcatcggcta 1320
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 Db 1321 aaggaattgggggtcctcctcctcctataagggtcacctctcagcacagagcctgatcatg 1380
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 QY 1381 ggaagagtcacacactcctgcacctgaagtactcctgccccacacctccttactgtggaaa 1440
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 Db 1381 ggaagagtcacacactcctgcacctgaagtactcctgccccacacctccttactgtggaaa 1440
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 |||
 Db 1501 attgggagagagcctccaccacccttgactcctcctatgaagcagctcgtgaattag 1560
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 |||
 Db 1561 ctactcaccaagagtgaggggacagagactccagtcacatgagtcctccagggcccttga 1620
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 Db 1621 tctgtacccccaccctatcctaaccaccaccttgctccactccagctccctgtattgat 1680
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 Db 1681 ataacctgtcaggtcgtgtggttacttgagggtcagagatagggaatccttat 1740
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 QY 1741 taaaactaacaatgaatatgtgtgttccatttcgaatttaataaagatacacaatg 1800
 |||
 Db 1741 taaaactaacaatgaatatgtgtgttccatttcgaatttaataaagatacacaatg 1800
 |||
 QY 1801 ttgtatgaaaaa 1813
 |||
 Db 1801 ttgtatgaaaaa 1813
 |||

RESULT 4
 AAS21412
 ID AAS21412 standard; cDNA; 1813 BP.

XX AC AAS21412;
 XX 24-OCT-2001 (first entry)
 DT
 XX
 DE Human cDNA sequence encoding for PRO246 polypeptide.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal

muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US32678.
 XX
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05601.
 PR 01-MAR-2000; 2000WO-US05004.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2001-408281/43.
 DR P-PSDB; AAU12340.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical -
 XX
 PS Claim 3; Fig 337; 813pp; English.
 XX
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing

PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor- α (TNF- α) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.

| | | | | |
|----------------------------|---------|--------------|--------|--------------|
| Query Match | 100.0%; | Score 1813; | DB 22; | Length 1813; |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | |
| Matches 1813; Conservative | 0; | Mismatches | 0; | Gaps |

Qy 1 ggagccgccctgggtgtcagcgcctcgcctccgcgcacgcctccggccgtcgcgcagcct 60
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Dd 1 ggagccgccctgggtgtcagcgcctcgcctccgcgcacgcctccggccgtcgcgcagcct 60

61 cggcacctgcaggtccgtccgcgagctgctgcgcccttgatccgtcccgccaaggga 12
|||||
61 cggcacctgcaggtccgtccgcgagctgctgcgcccttgatccgtcccgccaaggga 12

QY 121 gggccatgatctccctcccgggccctcgtgacaaacttgctgcgggttttgcctcg 18
|||||
121 gggccatgatctccctcccgggccctcgtgacaaacttgctgcgggttttgcctcg 18
|||||
Nb 121 gggccatgatctccctcccgggccctcgtgacaaacttgctgcgggttttgcctcg 18
|||||

181 ggctgaagtgcctcgagcccccctcgagggccagctgcaactgcaactgcccgcacc 24

241 ggttcgacgagcggtgagagaggggaagtgtgtctccagcgtgtacaccttgacgggg 30

301 aggtgtcttcacccacgacgcatggagtgcccttgtgatgtgttcttcaacagaaag 36

361 aaagaggatcaggtgtgtcctacatcaatgggtcacaacaaagcaaacctggagtat 42

421 ccttggtctaccatgacctcccggaactgtccctcgcgctggagggtctccagaga 48

QY 481 aagactctggccctacagctgtccgtgaattgtgcaagacaacaaggaatctaggg 540
|||||
Db 481 aagactctggccctacagctgtccgtgaattgtgcaagacaacaaggaatctaggg 540

[illegible]

```

801 gctccacagggcgcgcccaccgtcgaggccaatgcccaaacgaaga cga
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QY 661 gtaagcccgctgtccaataccagctgggatacggcagcttccatccctccagactttcttg 720
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Db 661 gtaagcccgctgtccaataccagctgggatacggcagcttccatccctccagactttcttg 720

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Oy 721 caccagcattagatgtcatccgtgggtctttaaaggcccaccaaacttcgtcttccaag 780
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Db 721 caccagcattagatgtcatccgtgggtctttaaaggcccaccaaacttcgtcttccaag 780

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QY      781 ctggaagtctatgtctgcgaagcccccaatgagtgggcactgcccaatgtaatgtagcg 840
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Db      781 ctggaagtctctgtccgcgaagcccacaatgatggtggcacctgcccaatgtaatgtagcg 840
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QY 841 tggagtgagcacagggcctggagcctgcagctggtctctggagctgtctgtggtaacctgg 900
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Db 841 tggagtgagcacagggcctggagcctgcagctggtctctggagctgtctgtggtaacctgg 900
|||||

QY 901 ttggaactggggctgctgctggcctgctcctctgtgtaacacagccggggcaagggccttgg 960
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Db 901 ttgaactgaagattgcctgaagctcgaagctgattcctcttgatccacacccggggcaagggccttga 960
|||||

OY

961 agagggccaaggcaatataacaaggagaagtgcctgctcccggaacctgccctgcccacaa 1020
|||||
DH 961 aaagaaccaccaaatatcgaagaagattgatcatgtccccgaactcacctaaccacaaa 1070
|||||

Qy 1021 agagctcagacacaatctccaagaatgggacccttcctctgcacctcgcagagccc 1080

QY 1081 tccggcaccaccccatggccctccacgggctgtgcatgacccccacggcccaftctctcca 1140
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Qy 1141 gccagcgccctgccctcaccaagactcggccacgacagatggggccaccctcaaccaatat 1200
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Qy 1201 cccccatccctgtgtggggtttctcctcctgtgcttgagcgcacatgggtgctgtgcctgtga 1260

1261 tggfgcctgcacgaagctcaagctgctctctgtafgatgaccccaactcaatggcta 1320

WD 1261 TGGTGTGCTGCACCAAGGTCATGCTCCTCGTGTAATGAATGACCACCATCATGTGGCTA 1320

DY 1321 AAGGATCTGGGTCCTCTCCTCTCTATAAGGTCACCTCTAGCACAGAAGCCCTGATCATG 1380

Db 1321 aaggattgggggtctctctctctataagggtcaacctctagacagaggcctgattcatg 1380
QY 1381 ggaagaagtcacactccttgacccttagtactctgccccaccctcttctactgtgggaaa 1440
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QY 1741 taaaactaacatgaatatgtgtgttctcatcttgcaaattaataaagatacataatg 1800
Db 1741 taaaactaacatgaatatgtgtgttctcatcttgcaaattaataaagatacataatg 1800
QY 1801 ttctgatgaaaaa 1813
Db 1801 ttctgatgaaaaa 1813

RESULT 5

AAF60372

ID AAF60372 standard; cDNA; 1813 BP.

XX AC AAF60372;

XX DT 27-APR-2001 (first entry)

XX DE PRO246 coding sequence.

KW Cytostatic; PRO protein; tumour; cancer; ss.

XX OS Homo sapiens.

PN WO200105836-A1.

PD 25-JAN-2001.

PF 20-DEC-1999; 99WO-US30999.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28564.
XX (GETH) GENENTECH INC.
XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
PI WPI; 2001-091968/10.
DR P-PSDB; AAB68599.
XX New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,
PT useful for diagnosing and treating cancers -
PS Claim 50; Fig 15; 196pp; English.
XX The present invention relates to PRO proteins and coding sequences. The
CC present sequence is the coding sequence for one such PRO protein.
CC It was found that the PRO genes are amplified in the genome of tumour
CC cells. The gene amplification is expected to be associated with the
CC overexpression of the gene product and contributes to tumourigenesis.
CC Therefore, antagonists of PRO proteins are useful for the treatment of
CC benign or malignant tumours, leukaemia, lymphoid malignancies and other
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
CC epithelial, inflammatory and immunologic disorders.
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 22; Length 1813;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps

0;

QY 1 ggaagccgctgggtgtcagcggctcggctcccgccagcgtccggcgtcgcgagcct 60

Db 1 ggaagccgctgggtgtcagcggctcggctcccgccagcgtccggcgtcgcgagcct 60

QY 61 cggcactgcaggtcgggtgcgtcccgcggtggtggcccttgactcgtcccgccaggg 120

Db 61 cggcactgcaggtcgggtgcgtcccgcggtggtggcccttgactcgtcccgccaggg 120

QY 121 gggccatgatccctcccgggggccctgtgtaaccaactgtgcggtttgttctctg 180

Db 121 gggccatgatccctcccgggggccctgtgtaaccaactgtgcggtttgttctctg 180

QY 181 ggtgagtgccctcgcccccctcgcgggcccgagctgcaactgcatctggccgaacc 240

Db 181 ggtgagtgccctcgcccccctcgcgggcccgagctgcaactgcatctggccgaacc 240

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Db 301 aggtgtcttcatcccgccatgaggagtgcccttctgtgatgtgtctctcaacagagaag 360
 Qy 361 aaaggaggtacaggtgtgtgtcctacatcaatgsggtcacacaagaacactgagtat 420
 Db 361 aaaggaggtacaggtgtgtgtcctacatcaatgsggtcacacaagaacactgagtat 420
 Qy 421 ccttggtctactccatgccccctccggaaacctgtccctgcggtggaagggtccagagaga 480
 Db 421 ccttggtctactccatgccccctccggaaacctgtccctgcggtggaagggtccagagaga 480
 Qy 481 aagactctggccctacagctgtccgtgaatgttgcaagacaacaaggcaaatctcaggg 540
 Db 481 aagactctggccctacagctgtccgtgaatgttgcaagacaacaaggcaaatctcaggg 540
 Qy 541 gccacagcatcaaaaaccttaagaactcaatgtactggttccctccagctcctccatcctgcc 600
 Db 541 gccacagcatcaaaaaccttaagaactcaatgtactggttccctccagctcctccatcctgcc 600
 Qy 601 gtctccaggtgtgtcccatgttgsgggcaaacgtgaacctgagctcagctctccaagga 660
 Db 601 gtctccaggtgtgtcccatgttgsgggcaaacgtgaacctgagctcagctctccaagga 660
 Qy 661 gtaagcccgctgtccaataccagtgsggtcggcagcttccatccttccagacttctcttg 720
 Db 661 gtaagcccgctgtccaataccagtgsggtcggcagcttccatccttccagacttctcttg 720
 Qy 721 caccagcatagatgtcatccgttgsggtctttaaagcctcaaccaacttctgtcttccatgg 780
 Db 721 caccagcatagatgtcatccgttgsggtctttaaagcctcaaccaacttctgtcttccatgg 780
 Qy 781 ctggaagtctatgtctgcaagggcccaaatgagtgsggcactgtcccaatgtaatgtcagcg 840
 Db 781 ctggaagtctatgtctgcaagggcccaaatgagtgsggcactgtcccaatgtaatgtcagcg 840
 Qy 841 tggaaagtgaacacagggcctcggaagctcgaatgtgtgtgctgsgagctgttgtgsgtaacctgg 900
 Db 841 tggaaagtgaacacagggcctcggaagctcgaatgtgtgtgctgsgagctgttgtgsgtaacctgg 900
 Qy 901 ttggaactggsggtgtgctggtcggtcggtctctctgtaccacgcggsggcaagggccctgg 960
 Db 901 ttggaactggsggtgtgctggtcggtcggtctctctgtaccacgcggsggcaagggccctgg 960
 Qy 961 aggaagccagccaatgatatacaaggaaggaatgcatgtctcccggaacctgtccctggccca 1020
 Db 961 aggaagccagccaatgatatacaaggaaggaatgcatgtctcccggaacctgtccctggccca 1020
 Qy 1021 agagctcagacacaatctccaagaatgggaaccttctctctgtcacctccgcacgagccc 1080
 Db 1021 agagctcagacacaatctccaagaatgggaaccttctctctgtcacctccgcacgagccc 1080
 Qy 1081 tccggccaccccatggccctcccgagcctgtgcatctgaacccccaagcccaagtctctcca 1140
 Db 1081 tccggccaccccatggccctcccgagcctgtgcatctgaacccccaagcccaagtctctcca 1140
 Qy 1141 gccaggccctgtccctcaccaagaactgcacgacagatggggcccaacctcaacaatat 1200
 Db 1141 gccaggccctgtccctcaccaagaactgcacgacagatggggcccaacctcaacaatat 1200

Qy 1201 cccccatcccttggtaggggttcttctcctctggttagccgcatgggtgtgtgtga 1260
 Db 1201 cccccatcccttggtaggggttcttctcctctggttagccgcatgggtgtgtgtga 1260
 Qy 1261 tggtagtggccagagtcgaagctggtctctctgtatgatgacccaccatcattgtgcta 1320
 Db 1261 tggtagtggccagagtcgaagctggtctctctgtatgatgacccaccatcattgtgcta 1320
 Qy 1321 aagatttggsggtctctccttccataaagggtcacctctagacagagggcctgagtcagt 1380
 Db 1321 aagatttggsggtctctccttccataaagggtcacctctagacagagggcctgagtcagt 1380
 Qy 1381 ggaagaagtcacactcctgaacctagtaactctgccccaccctcttactgtggaaa 1440
 Db 1381 ggaagaagtcacactcctgaacctagtaactctgccccaccctcttactgtggaaa 1440
 Qy 1441 accatctcagtaagacctaagtgtccaggagacagaaggagagaagtgtgattcgtga 1500
 Db 1441 accatctcagtaagacctaagtgtccaggagacagaaggagagaagtgtgattcgtga 1500
 Qy 1501 attggagaggagctccaccaccctgactcctccttatgaagccagctgtcgaatatag 1560
 Db 1501 attggagaggagctccaccaccctgactcctccttatgaagccagctgtcgaatatag 1560
 Qy 1561 ctactcaccaagagtgaaggggcagagactccagtcactgagctcccaagcccccctga 1620
 Db 1561 ctactcaccaagagtgaaggggcagagactccagtcactgagctcccaagcccccctga 1620
 Qy 1621 tctgtacccccaccctcttcaacaccacccttggctccaccctcagctccctgtatgat 1680
 Db 1621 tctgtacccccaccctcttcaacaccacccttggctccaccctcagctccctgtatgat 1680
 Qy 1681 ataactgttcaggctggtgtgttaagtttcaactgsgggcagagataggaaatctcttat 1740
 Db 1681 ataactgttcaggctggtgtgttaagtttcaactgsgggcagagataggaaatctcttat 1740
 Qy 1741 taaactcaacatgaatatgtgtgtttcatttcaatttcaaatataaagatacatatgt 1800
 Db 1741 taaactcaacatgaatatgtgtgtttcatttcaatttcaaatataaagatacatatgt 1800
 Qy 1801 ttgtatgaaaaa 1813
 Db 1801 ttgtatgaaaaa 1813

RESULT 6
 AAC87040
 ID AAC87040 standard; cDNA; 1813 BP.
 XX
 AC AAC87040;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of human polypeptide PRO246.
 XX
 KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
 KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361;
 PRO1308;

Qy 481 aagactctgccccctacagctgcctccgtgaatgtgtgaagaacaacaaggcaaatctaggg 540
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 Db 481 aagaactctgccccctacagctgcctccgtgaatgtgtgaagaacaacaaggcaaatctaggg 540
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 Qy 541 gccacagcatcaaaacctagaactcaatgtaactgtctcctccagctcctccatccctggc 600
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 Db 541 gccacagcatcaaaacctagaactcaatgtaactgtctcctccagctcctccatccctggc 600
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 Qy 601 gtctccagggtgtgcccccatgttgggggcaaacgtgaacctgtgagctgcagctctccaagg 660
 |||
 Db 601 gtctccagggtgtgcccccatgttgggggcaaacgtgaacctgtgagctgcagctctccaagg 660
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 Qy 661 gtaagccgcgtgtccaataccagtggaatcggaagcttccalcctccaagaatttcttgg 720
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 Db 661 gtaagccgcgtgtccaataccagtggaatcggaagcttccalcctccaagaatttcttgg 720
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 Qy 721 caccagcattagatgtcatccgttgggtctttaagcctcaccaaccttgcgtcttccatgg 780
 |||
 Db 721 caccagcattagatgtcatccgttgggtctttaagcctcaccaaccttgcgtcttccatgg 780
 |||
 Qy 781 ctggaagtctatgtctgtcaaggcccaaatgaagtggaagctgcaccaatgtatgtacgc 840
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 Db 781 ctggaagtctatgtctgtcaaggcccaaatgaagtggaagctgcaccaatgtatgtacgc 840
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 Qy 841 tggaaagtgaacacaaggccttgagctgcagtggtgtgtgagagctgtgttgggtaccctgg 900
 |||
 Db 841 tggaaagtgaacacaaggccttgagctgcagtggtgtgtgagagctgtgttgggtaccctgg 900
 |||
 Qy 901 ttggaactgggggtgtgctggcttgggtctgtccctctgtaccacccgcgggggcaaggccctgg 960
 |||
 Db 901 ttggaactgggggtgtgctggcttgggtctgtccctctgtaccacccgcgggggcaaggccctgg 960
 |||
 Qy 961 aggaagccagccaatgatatacaaggagatgcattgtctcccgagaccctggccttggccca 1020
 |||
 Db 961 aggaagccagccaatgatatacaaggagatgcattgtctcccgagaccctggccttggccca 1020
 |||
 Qy 1021 agagctcagacaacaatctccaagaatggagacccttctcctgtcacctccgcagagccc 1080
 |||
 Db 1021 agagctcagacaacaatctccaagaatggagacccttctcctgtcacctccgcagagccc 1080
 |||
 Qy 1081 tccggccaacccaatggcctccccaagcctgtgtgcatgtgacccccacagcccaagtctctcca 1140
 |||
 Db 1081 tccggccaacccaatggcctccccaagcctgtgtgcatgtgacccccacagcccaagtctctcca 1140
 |||
 Qy 1141 gccaggccccgcctcaccacaagatgcccacagacagatggggccaccctcaaccaatat 1200
 |||
 Db 1141 gccaggccccgcctcaccacaagatgcccacagacagatggggccaccctcaaccaatat 1200
 |||
 Qy 1201 cccccatccctgttgggggtctctcctctgtgcttgagccgcatgggtgtgtgcctgtga 1260
 |||
 Db 1201 cccccatccctgttgggggtctctcctctgtgcttgagccgcatgggtgtgtgcctgtga 1260
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 Qy 1261 tgggtcctgcctcagaagtcagaagctgtctctgtgatgatgacccccacatcatgtgcta 1320
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 Db 1261 tgggtcctgcctcagaagtcagaagctgtctctgtgatgatgacccccacatcatgtgcta 1320
 |||
 Qy 1321 aaggattgggggtctctcctctctataagggtcacacttagcacagaggccttgatcatg 1380
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Db 1321 aaggattgggggtctctcctctctataagggtcacacttagcacagaggccttgatcatg 1380
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 Qy 1381 ggaagaagtcacactcctgaacccttagtactctgcccacactctcttactgtggaaa 1440
 |||
 Db 1381 ggaagaagtcacactcctgaacccttagtactctgcccacactctcttactgtggaaa 1440
 |||
 Qy 1441 accatctcagtaagaacctaaagtgtccaggagacagaaggagagaagtgatgtcgg 1500
 |||
 Db 1441 accatctcagtaagaacctaaagtgtccaggagacagaaggagagaagtgatgtcgg 1500
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 Qy 1501 attggaggagcctccaccacccctgaactcctcctatgaagccagctgtcgaatatg 1560
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 Db 1501 attggaggagcctccaccacccctgaactcctcctatgaagccagctgtcgaatatg 1560
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 Qy 1561 ctactccaagaagtgaggggcagagaactccagtcactgaagctccagggcccttga 1620
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 Db 1561 ctactccaagaagtgaggggcagagaactccagtcactgaagctccagggcccttga 1620
 |||
 Qy 1621 tctgtaccccaacctctataaccaccccttggctcccaactccagctccctgtatgat 1680
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 Db 1621 tctgtaccccaacctctataaccaccccttggctcccaactccagctccctgtatgat 1680
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 Qy 1681 ataactgtcagagctggctgtgttaggttttaactggggcagagataggaaatctctat 1740
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 Db 1681 ataactgtcagagctggctgtgttaggttttaactggggcagagataggaaatctctat 1740
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 Qy 1741 taaactaacatgaataatgtgtgtttcatattgcaaatttaataagaatacatatg 1800
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 Db 1741 taaactaacatgaataatgtgtgtttcatattgcaaatttaataagaatacatatg 1800
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 Qy 1801 ttgtatgaaaaa 1813
 |||
 Db 1801 ttgtatgaaaaa 1813
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RESULT 7
 AAF72379
 ID AAF72379 standard; cDNA; 1813 BP.
 XX
 AC AAF72379;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human PRO246 cDNA.
 XX
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
 KW antiarthritic; antiinfertility; anti diabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation; se.
 XX
 OS Homo sapiens.
 XX
 PN WO200104311-A1.
 XX
 PD 18-JAN-2001.
 XX

Qy 901 ttggactggggttgccggtctgggtccctcttgtaaccaccgcccggggcaggccctgg 960
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 Db 901 ttggactggggttgctggctgggctgggtccctcttgtaaccaccgcccggggcaggccctgg 960
 Qy 961 aggaagccagccaatgatatcaagagagatgcatctgctcccggaacctggccctggccca 1020
 |||||
 Db 961 aggaagccagccaatgatatcaagagagatgcatctgctcccggaacctggccctggccca 1020
 Qy 1021 agagctcagacaacaatctccaagaatgggaacctcttctctgtcaacctccgcaagagccc 1080
 |||||
 Db 1021 agagctcagacaacaatctccaagaatgggaacctcttctctgtcaacctccgcaagagccc 1080
 Qy 1081 tccggccaaccccatgacctcccaaggcctgggtgcatctgaccccaagcccaagctctcca 1140
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 Db 1081 tccggccaaccccatgacctcccaaggcctgggtgcatctgaccccaagcccaagctctcca 1140
 Qy 1141 gccaggccctgcctcccaaccaagactgcccaagacagatggggcccaacctcaaccaatat 1200
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 Db 1141 gccaggccctgcctcccaaccaagactgcccaagacagatggggcccaacctcaaccaatat 1200
 Qy 1201 ccccatcctgtgtgggtctctcctctgacctgagccgcagtggtgtgctgtga 1260
 |||||
 Db 1201 ccccatcctgtgtgggtctctcctctgacctgagccgcagtggtgtgctgtga 1260
 Qy 1261 tggctcgtgccagagtcgaagctggtctctgtgatgagcccaactcatctgcta 1320
 |||||
 Db 1261 tggctcgtgccagagtcgaagctggtctctgtgatgagcccaactcatctgcta 1320
 Qy 1321 aaggattgggggtctctcctcctctataagggtcaacctctaacacaaaggcctgagtcagt 1380
 |||||
 Db 1321 aaggattgggggtctctcctcctcctataagggtcaacctctaacacaaaggcctgagtcagt 1380
 Qy 1381 ggaagagtcacactcctgaacctgaactctgcccccaacctcttctactgtgggaaa 1440
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 Db 1381 ggaagagtcacactcctgaacctgaactctgcccccaacctcttctactgtgggaaa 1440
 Qy 1441 accatctcagtaagaactaagtgtccaggagacagaaggagaaggaagtggatctgga 1500
 |||||
 Db 1441 accatctcagtaagaactaagtgtccaggagacagaaggagaaggaagtggatctgga 1500
 Qy 1501 attgggagagagcctccacacacccctgacctcctctatgaagccagctgctgaattag 1560
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 Db 1501 attgggagagagcctccacacacccctgacctcctctatgaagccagctgctgaattag 1560
 Qy 1561 ctactcaccaagagtgaggggcagagactccagtcactgaagtcctccagagccctctga 1620
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 Db 1561 ctactcaccaagagtgaggggcagagactccagtcactgaagtcctccagagccctctga 1620
 Qy 1621 tctgtaccccaacctatctaacaccacaccttgctcccaactccagctccctgtatgat 1680
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 Db 1621 tctgtaccccaacctatctaacaccacaccttgctcccaactccagctccctgtatgat 1680
 Qy 1681 ataacctgtcagctggtgtgtgtgttacttggggcagagatagggaaatctcttat 1740
 |||||
 Db 1681 ataacctgtcagctggtgtgtgtgttacttggggcagagatagggaaatctcttat 1740
 Qy 1741 taaaactaacatgaatatgtgtgttttccatttgcgaatttaataagaatacataatg 1800
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Db 1741 taaaactaacatgaatatgtgtgttttccatttgcgaatttaataagaatacataatg 1800
 Qy 1801 ttgtatgaaaaa 1813
 |||||
 Db 1801 ttgtatgaaaaa 1813
 RESULT 8
 AAC97441
 ID AAC97441 standard; cDNA; 1813 BP.
 XX
 AC AAC97441;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human angiogenesis-associated protein PRO246 cDNA, SEQ ID NO:95.
 XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal; ss.
 XX
 OS Homo sapiens.
 OS
 XX
 PN WO200053753-A2.
 XX
 PD 14-SEP-2000.
 XX
 PE 05-JAN-2000; 2000WO-US00219.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsden SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WJ;
 XX
 DR WPI; 2001-090793/10.
 DR P-PSDB; AAB53082.

Db 961 aggagccagccaatgatatacaaggagatgccattgtctcccggaacctgtgcccctgtgccc 1020

QY 1021 agagctcagacacaatctccaagaatggagaccttctctgtcacctccgcagagccc 1080

Db 1021 agagctcagacacaatctccaagaatggagaccttctctgtcacctccgcagagccc 1080

QY 1081 tccggccaccatgtgacctcccaaggctgtgtcatgtgacccccaagccagctctctcca 1140

Db 1081 tccggccaccatgtgacctcccaaggctgtgtcatgtgacccccaagccagctctctcca 1140

QY 1141 gccagggccctgacctcaaccaagactgccacagacagatggggcccaacctcaaccaatat 1200

Db 1141 gccagggccctgacctcaaccaagactgccacagacagatggggcccaacctcaaccaatat 1200

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QY 1261 tgggtgctgccccagagtcaagctgctctctgtatgatgaccccaacctattgtgcta 1320

Db 1261 tgggtgctgccccagagtcaagctgctctctgtatgatgaccccaacctattgtgcta 1320

QY 1321 aaggaattgggggtctctctctctataaagggtcacctctagcacagaggcctgagtcata 1380

Db 1321 aaggaattgggggtctctctctctataaagggtcacctctagcacagaggcctgagtcata 1380

QY 1381 ggaagagtcacacitcctgacctagctactctgccccacctctcttactgtgggaaa 1440

Db 1381 ggaagagtcacacitcctgacctagctactctgccccacctctcttactgtgggaaa 1440

QY 1441 accatctcagtaagacctaaagtgtccaggagacagaaggagaagagtgatctgta 1500

Db 1441 accatctcagtaagacctaaagtgtccaggagacagaaggagaagagtgatctgta 1500

QY 1501 attggagagagcctccaccaccctgacctctctctatgaagccagctgtctgaattag 1560

Db 1501 attggagagagcctccaccaccctgacctctctctatgaagccagctgtctgaattag 1560

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Db 1561 ctactccaccaagatgagaggggcagagacttccagtcactgagctcccaagcccccttga 1620

QY 1621 tctgtacccccaccctatctaaccaccacctgtgtccactccagctccctgtatgat 1680

Db 1621 tctgtacccccaccctatctaaccaccacctgtgtccactccagctccctgtatgat 1680

QY 1681 ataacctgtcaggtgtgtgtgtgtgtttactctggtgggcagagatagggaatctcttat 1740

Db 1681 ataacctgtcaggtgtgtgtgtgtgtttactctggtgggcagagatagggaatctcttat 1740

QY 1741 taaaactaacaatgaatatgtgtgtttcatttgcacaatttaaataaagatacataatg 1800

Db 1741 taaaactaacaatgaatatgtgtgtttcatttgcacaatttaaataaagatacataatg 1800

QY 1801 ttgtatgaaaaa 1813

Db 1801 ttgtatgaaaaa 1813

RESULT 9

AAFP93785

ID AAFP93785 standard; cDNA; 1821 BP.

XX

AC AAFP93785;

XX

DT 23-MAY-2001 (first entry)

XX

DE Human cDNA encoding a membrane or secretory protein clone PSEC0086.

XX

KW Human; secretory protein; membrane protein; vaccine; gene therapy;

KW rheumatoid arthritis; diabetes; as.

XX

OS Homo sapiens.

XX

PN EP1067182-A2.

XX

PD 10-JAN-2001.

XX

PF 07-JUL-2000; 2000EP-0114090.

XX

PR 08-JUL-1999; 99JP-0194179.

PR 11-JAN-2000; 2000JP-0118775.

PR 02-MAY-2000; 2000JP-0183766.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX

DR WPI; 2001-093989/11.

DR P-PSDB; AAB88358.

XX

PT Nucleic acids encoding secretory proteins/membrane proteins, useful in

PT gene therapy or as candidate target molecules in drug development -

XX

PS Claim 1; SEQ ID 83; 609pp + CD ROM; English.

XX

CC This invention relates to nucleic acid sequences AAFP93744 - AAFP93916

CC which encode human secretory or membrane proteins represented by

CC AAB88317 - AAB88419. Included in the invention are primers

CC AAFP93917 - AAFP94295 and AAFP62232 - AAFP62235 which are used to isolate

the

CC cDNA sequences of the invention. The invention also includes methods for

CC the production of antibodies directed against the proteins, and cDNA

CC sequences, which can be used in vaccines. The polynucleotide sequences

CC can be used in gene therapy. The polynucleotide sequences and the

CC proteins they encode may be used in the prevention, treatment and

CC diagnosis of diseases associated with inappropriate secretory

CC protein/membrane protein expression. The nucleic acids and complementary

CC sequences may also be used as DNA probes in diagnostic assays

CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the

CC presence of similar nucleic acid sequences in samples. They may also be

CC used to study the expression and function of secretory proteins/membrane

CC polypeptides and their role in metabolism. The polypeptides may be used

CC as antigens in the production of antibodies against them and in assays

to

CC identify modulators (agonists and antagonists) of expression and

CC activity. The antibodies and antagonists may also be used as therapeutic

CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.

XX Sequence 1821 BP; 366 A; 561 C; 489 G; 405 T; 0 other;

Query Match 99.8%; Score 1809; DB 22; Length 1821;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1809; Conservative 0; Mismatches 0; Indels 0; Gaps

0;

QY 1 ggaagccgcctgggtgtcagcggtcggctcccgcgcaagctccggcctgcgcagacct 60

Db 12 ggaagccgcctgggtgtcagcggtcggctcccgcgcaagctccggcctgcgcagacct 71

QY 61 cggcacctgcaggtccggtgcgtccgcgcgtggcgccctgaactccgtcccgccagggga 120

Db 72 cggcacctgcaggtccggtgcgtccgcgcgtggcgccctgaactccgtcccgccagggga 131

QY 121 gggccatgatctccctccggggccctcgtgtgacccaactgtgcggttttctcctgg 180

Db 132 gggccatgatctccctccggggccctcgtgtgacccaactgtgcggttttctcctgg 191

QY 181 ggcgtggtgcctcgcgcgcctccgcgcgcgcagctgcaactgcaacttgcgcgcaacc 240

Db 192 ggcgtggtgcctcgcgcgcctccgcgcgcgcagctgcaactgcaacttgcgcgcaacc 251

QY 241 ggttcgacggcgggtgagggagggaggtgtgtcttcacgcgtgtgtacaccttgcacgggg 300

Db 252 ggttcgacggcgggtgagggagggaggtgtgtcttcacgcgtgtgtacaccttgcacgggg 311

QY 301 aggtgtctcatccacgcatgggaggtgacctgtgtatgtgtcttcaacagagaag 360

Db 312 aggtgtctcatccacgcatgggaggtgacctgtgtatgtgtcttcaacagagaag 371

QY 361 aaaaggaagatcaggtgttctcctacatcaatgsggtcacacaagcaaacctgagtat 420

Db 372 aaaaggaagatcaggtgttctcctacatcaatgsggtcacacaagcaaacctgagtat 431

QY 421 ccttggtctactccatgcccctccgggaacctgtccctgcggtgaggggtctccagaga 480

Db 432 ccttggtctactccatgcccctccgggaacctgtccctgcggtgaggggtctccagaga 491

QY 481 aagaccttggccctcctacagctgtccgtgaatgtgcagaacaagaagcaatctcagg 540

Db 492 aagaccttggccctcctacagctgtccgtgaatgtgcagaacaagaagcaatctcagg 551

QY 541 gccacagcatcaaaaccttagaactcaatgtactggttccctccagctcctccatcctgcc 600

Db 552 gccacagcatcaaaaccttagaactcaatgtactggttccctccagctcctccatcctgcc 611

QY 601 gtctccaggggtgtgcccacatgtgggggcaaacgtgacccctgagctgcaggtctccaagga 660

Db 612 gtctccaggggtgtgcccacatgtgggggcaaacgtgacccctgagctgcaggtctccaagga 671

QY 661 gtaagcccgctgtccaataccggtggtatcggcagcttccatcctccagacttctcttg 720

Db 672 gtaagcccgctgtgtccaataccggtggtatcggcagcttccatcctccagacttctcttg 731

QY 721 caccagcatatgatgtcatccgtgggtctttaagccccaacacttctgtctccatgg 780

Db 732 caccagcatatgatgtcatccgtgggtctttaagccccaacacttctgtctccatgg 791

QY 781 ctggagttctatgtctgcaaggcccaatgaagtgggacatgcccatagtatgtagcc 840

Db 792 ctggagttctatgtctgcaaggcccaatgaagtgggacatgcccatagtatgtagcc 851

QY 841 tggaaagtgaacacagggcctggagctgagctgtgtcgtgagactgtgtggttaccctgg 900

Db 852 tggaaagtgaacacagggcctggagctgagctgtgtcgtgagactgtgtggttaccctgg 911

QY 901 ttggactgggggtgtgtcgtggtggtgtgtcctctgttaccacgcgcggggcaaggccctgg 960

Db 912 ttggactgggggtgtgtcgtggtggtgtgtcctctgttaccacgcgcggggcaaggccctgg 971

QY 961 aggaagccagccaatgatatacaaggagatgcatgtctcccggaacctgtccctgtgccca 1020

Db 972 aggaagccagccaatgatatacaaggagatgcatgtctcccggaacctgtccctgtgccca 1031

QY 1021 agagctcagacaacaatctccaagaatggagaccttccctgtgcacctccgacagagccc 1080

Db 1032 agagctcagacaacaatctccaagaatggagaccttccctgtgcacctccgacagagccc 1091

QY 1081 tccggccaaccccatgacctcccaaggcctgtgtgcatgagccccacgcgcagctctcca 1140

Db 1092 tccggccaaccccatgacctcccaaggcctgtgtgcatgagccccacgcgcagctctcca 1151

QY 1141 gccagggcctgtgcctcaccaagaactgcccacgacagatgggggcccaacctcaaccaatat 1200

Db 1152 gccagggcctgtgcctcaccaagaactgcccacgacagatgggggcccaacctcaaccaatat 1211

QY 1201 cccccatccctgtgtggggttctctcctctgtgcttgagccgcatggtgtgcctgtga 1260

Db 1212 cccccatccctgtgtggggttctctcctctgtgcttgagccgcatggtgtgcctgtga 1271

QY 1261 tgggtgcctggccagagtcgaagctggtctctgtgatgatgaccccaacctcatgtgcta 1320

Db 1272 tgggtgcctggccagagtcgaagctggtctctgtgatgatgaccccaacctcatgtgcta 1331

QY 1321 aaggatttggggtctctcccttccatataaggtgcacctctagcacagagggcctgagtcatg 1380

Db 1332 aaggatttggggtctctcccttccatataaggtgcacctctagcacagagggcctgagtcatg 1391

QY 1381 ggaaagagtcacacctcctgacaccttagtactgtgcccccaacctctcttactgtgggaaa 1440

Db 1392 ggaaagagtcacacctcctgacaccttagtactgtgcccccaacctctcttactgtgggaaa 1451

QY 1441 accatctcagttaagaccttaagtgtccaggagacagaaaggaggaaggaagtgtgactctgga 1500

Db 1452 accatctcagttaagaccttaagtgtccaggagacagaaaggaggaaggaagtgtgactctgga 1511

QY 1501 attggsggagagcttcaaccacacctgtactcctccttatgaagccagctgtcgaatatag 1560

Db 1512 attggaggagcctccaccacccttgactcctccttatgaagccagctgctgaattag 1571
Qy 1561 ctactaccaagagtgagggcagagactcctcagtcagtgaagtcctccaggcccttga 1620
Db 1572 ctactaccaagagtgagggcagagactcctcagtcagtgaagtcctccaggcccttga 1631
Qy 1621 tctgtacccacccttatctaacaccacccttgctcccaactccagctccctgtatgat 1680
Db 1632 tctgtacccacccttatctaacaccacccttgctcccaactccagctccctgtatgat 1691
Qy 1681 ataactgtcaggtcgtgctgtgagtttactggggcagagatagggaattccttat 1740
Db 1692 ataactgtcaggtcgtgctgtgagtttactggggcagagatagggaattccttat 1751
Qy 1741 taaactaacatgaatatgtgtgttctcatcttgcaaatataaagaatacataatg 1800
Db 1752 taaactaacatgaatatgtgtgttctcatcttgcaaatataaagaatacataatg 1811
Qy 1801 ttgtcatga 1809
Db 1812 ttgtcatga 1820

RESULT 10
AAH02949

ID AAH02949 standard; DNA; 1827 BP.
XX
AC AAH02949;
XX
DT 15-JUN-2001 (first entry)
XX
DE Human shear stress-response coding sequence SEQ ID NO: 143.
XX
KW Human; shear stress-response protein; vascular disease;
KW arteriosclerosis; ds.
XX
OS Homo sapiens.
XX
PN WO200125427-A1.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-JP06840.
XX
PR 01-OCT-1999; 99JP-0280976.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJI/) NOJIMA H.
XX
PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
XX
DR WPI; 2001-266308/27.
DR P-PSDB; AAB90818.
PT DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis -

XX
PS Claim 1; Page 595-599; 678bp; Japanese.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension.
XX
SQ Sequence 1827 BP; 369 A; 559 C; 491 G; 408 T; 0 other;

Query Match 99.6%; Score 1806.6; DB 22; Length 1827;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 4; Indels 0; Gaps

Qy 1 ggagccgcccctgggtgtgtcagcggctcggctcccgcgacgctccggccgtcggcagcct 60
Db 13 ggagccgcccctgggtgtgtcagcggctcggctcccgcgacgctccggccgtcggcagcct 72
Qy 61 cggcacctgcaggtccggtcgtcccgcgctggcgccccctgactccgtcccgccagggga 120
Db 73 cggcacctgcaggtccggtcgtcccgcgctggcgccccctgactccgtcccgccagggga 132
Qy 121 ggagccatgatccctcccgccgggccccctgtgaccaaactgtgcgattttgtcctcg 180
Db 133 ggagccatgatccctcccgccgggccccctgtgaccaaactgtgcgattttgtcctcg 192
Qy 181 ggctgagtgccctgcgcgcccccctgcgcggccagctgcgaactgtgcccgcgaacc 240
Db 193 ggctgagtgccctgcgcgcccccctgcgcggccagctgcgaactgtgcccgcgaacc 252
Qy 241 ggttcgagcggttggaaggaggggaagtgtgtctccagcgtgtgtacaccttgcagggg 300
Db 253 ggttcgagcggttggaaggaggggaagtgtgtctccagcgtgtgtacaccttgcagggg 312
Qy 301 aggtgtcttcatcccaagcatgggaagtgtcccttgtgatgtgttcttcaacagaaga 360
Db 313 aggtgtcttcatcccaagcatgggaagtgtcccttgtgatgtgttcttcaacagaaga 372
Qy 361 aaaaggagatcaggtgtgtcctacatcaatggggtccacaagaagcaaacctggagrat 420
Db 373 aaaaggagatcaggtgtgtcctacatcaatggggtccacaagaagcaaacctggagrat 432
Qy 421 cctgtgtactccatcgccctcccggaacctgtccctgcgctggaggggtcccaaggaga 480
Db 433 cctgtgtactccatcgccctcccggaacctgtccctgcgctggaggggtcccaaggaga 492
Qy 481 aagactctggcccctacagctgtccgtgaatgtgcagaagacaagaaggcaaatctaagg 540
Db 493 aagactctggcccctacagctgtccgtgaatgtgcagaagacaagaaggcaaatctaagg 552
Qy 541 gccacagcatcaaaaccttagaactcaatgttactgtgttctccagctcctccatctctg 600
Db 553 gccacagcatcaaaaccttagaactcaatgttactgtgttctccagctcctccatctctg 612
Qy 601 gtctccaggtgtgtcccatgtgggggcaaacgltgacaccttgagctgcagctcctcaagg 660

Db 613 gtctccagggtgtgcccccatgtgggggcaaacgtgacctgagctgcgcagctctccaaggaa 672
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 QY 721 caaccagcatatgatatgtcatccgltgggtctttaagcctcaaccaacttctgtcttccatgg 780
 Db 733 caccagcatatgatatgtcatccgltgggtctttaagcctcaaccaacttctgtcttccatgg 792
 QY 781 ctggagctatagtctgtgcaaggcccaacaatgaggtgggcacgtgcccaatgttaatgtgagc 840
 Db 793 ctggagctatagtctgtgcaaggcccaacaatgaggtgggcacgtgcccaatgttaatgtgagc 852
 QY 841 tggaaagtgaagacagaggccttgagctgcagctggtgtgtgtgagagctgtgtggtaacctgg 900
 Db 853 tggaaagtgaagacagaggccttgagctgcagctggtgtgtgtgagagctgtgtggtaacctgg 912
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 Db 973 agggagccagccaatgatataccaaggagagtgccatgtctccccgagacctggccctggccca 1032
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 QY 1741 taaacctacaatgaataatgtgtgtttcatttgcataattcaataagaatacataatg 1800
 Db 1753 taaacctacaatgaataatgtgtgtttcatttgcataattcaataagaatacataatg 1812
 QY 1801 ttgtatgaaaaa 1813
 Db 1813 ttgtatgagata 1825
 RESULT 11
 AAD12605
 ID AAD12605 standard; cDNA; 1816 BP.
 XX
 AC AAD12605;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Human protein having hydrophobic domain encoding cDNA clone HP10801.
 XX
 KW Human; hydrophobic domain; gene therapy; nutritional supplement;
 KW cell proliferation; immunomodulatory; autoimmune disorder;
 KW antimicrobial;
 KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
 KW haemotopiasis; tissue growth activity; Parkinson's disease; cytostatic;
 KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
 KW contraceptive; antiinfertility; antiinflammatory; ss.
 OS Homo sapiens.
 XX
 FH Key
 FT CDS
 FT /tag= a
 FT /product= "Human protein having hydrophobic domain"
 FT /note= "CDS is specifically is claimed in claim 3"
 FT sig_peptide
 FT /tag= b
 FT /tag= 134..223
 FT mat_peptide
 FT /tag= 224..1303
 FT /tag= c
 FT /product= "Mature human protein with hydrophobic domain"
 XX
 PN WO200149728-A2.

Db 849 tggaaagtgaagcaacaggccttgagctgcagtcggttgctgagagctgtgtgggtacccttg 908
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Db 909 ttggactggggttgcctggctgggctggtcctcttgtaaccactgcggggcaaggcccttg 968
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Qy 1741 taaactaacatgaatatgtgtgtttcatttgcacaatttaataagaatacataatg 1800
Db 1749 taaactaacatgaatatgtgtgtttcatttgcacaatttaataagaatacataatg 1808
Qy 1801 ttgtgatg 1808
Db 1809 ttgtgatg 1816

RESULT 12

AAA23441
ID AAA23441 standard; cDNA; 1954 BP.

AC AAA23441;

DT 19-JUN-2000 (first entry)

DE cDNA encoding human secreted protein vc51_1, SEQ ID NO:37.

KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive; ss.

OS Homo sapiens.

FN Key Location/Qualifiers
FT CDS 139..1311
FT /tag= a
FT /product= "Human secreted protein vc51_1"

PN WO200011015-A1.

XX 02-MAR-2000.

PF 24-AUG-1999; 99WO-US19351.

XX 24-AUG-1998; 98US-0097638.

PR 24-AUG-1998; 98US-0097659.

PR 09-SEP-1998; 98US-0099618.

PR 28-SEP-1998; 98US-0102092.

PR 25-NOV-1998; 98US-0109978.

PR 23-DEC-1998; 98US-0113645.

PR 23-DEC-1998; 98US-0113646.

PR 23-AUG-1999; 99US-0379246.

PA (ALPH-) ALPHAGENE INC.

PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

DR WPI; 2000-224657/19.

DR P-PSDB; AAY94999.

PT New secreted or transmembrane proteins and polynucleotides encoding
PT them, useful for treating neurodegenerative disorders, autoimmune
PT diseases and cancer -

XX Claim 46; Page 296; 357pp; English.

XX The invention relates to 40 human secreted proteins (AAV94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
CC proteins of the invention include those that are thought to be only
CC partially secreted, i.e., transmembrane proteins. The proteins of the
CC invention may exhibit one or more activities selected from the
following:
CC cytokine activity; cell proliferation; differentiation; immune
CC modulation; haematopoiesis regulation; tissue growth activity;
CC activation/inhibin activity; chemotactic/chemokinetic activity; haemostatic
CC and thrombolytic activity; anti-inflammatory activity; and tumour
CC inhibition activity. The proteins may be administered to patients as
CC vaccines, and the nucleotides may be used as part of a gene therapy
CC regime. Diseases or conditions that may be treated using the proteins or
CC nucleotides of the invention include autoimmune diseases; genetic
CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
CC fungal and viral infections, especially HIV; multiple sclerosis;
CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
CC insulin dependent diabetes mellitus; and allergic reactions such as
CC asthma and anaemia. They may also be used for treating wounds, burns,
CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease and amyotrophic
CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may be
CC additionally be useful as contraceptives. Nucleic acid sequences of the
CC invention may be used in chromosome mapping, and as a source of
CC diagnostic primers and probes. The present sequence represents cDNA
CC encoding one of the 40 proteins of the invention.

XX Sequence 1954 BP; 498 A; 561 C; 490 G; 405 T; 0 other;

Query Match 99.4%; Score 1802; DB 21; Length 1954;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1813; Conservative 0; Mismatches 0; Indels 1; Gaps

1;
QY 1 ggagccgcccgtggtcagc-ggctcgctcccgcgcaagctccggcgtcgcgacgc 59
Db 13 ggagccgcccgtggtcagcgggctcgctcccgcgcaagctccggcgtcgcgacgc 72
QY 60 tcggcaactgcaagtcctgctgcgtcccgcgagctgscgcccctgactccgtcccgcaagg 119
Db 73 tcgcaactgcaagtcctgctgcgtcccgcgagctgscgcccctgactccgtcccgcaagg 132
QY 120 agggcatgatcttcctcccgggggcccctggtgaccaactgctgcggttttgcctg 179
Db 133 agggcatgatcttcctcccgggggcccctggtgaccaactgctgcggttttgcctg 192
QY 180 gggctgagtgccctcgcgccccctcggggccagctgcaactgcaactgcccccaac 239
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Db 253 cggctgcagcgcggtggaagggaagggaagtgtgtcttcacagctgtgacacctgcaagg 312
QY 300 gagtgtcttcacccagcatgggaggtgcacctgtgatgtgtgtcttcaaacagaa 359

Db 313 gagggtcttcacccagcatgggaggtgcccttgatgtgtgtcttcaaacagaa 372
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QY 420 tccttgctactcatcgccctcccggaacctgtccctgcggtggaagggtctccaggag 479
Db 433 tccttgctactcatcgccctcccggaacctgtccctgcggtggaagggtctccaggag 492
QY 480 aaagactctggccccctacagctgtccgtgaatgtgcaagacaacaaggcaaatcagg 539
Db 493 aaagactctggccccctacagctgtccgtgaatgtgcaagacaacaaggcaaatcagg 552
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Db 553 ggccacagcatcaaaaccttagaactcaatgtracgtgttcctccagctctccatcctgc 612
QY 600 cgtctccaggtgtgccccatgctgggggcaaacgtgtaacctgagctgcagctccaagg 659
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 Db 1213 tccccatccctggtggggttctctctctgcttgaagccgcatgggtgctgctgtg 1272
 QY 1260 atggtgctgcccagagtcgaagctggctctctggtatgatgacccaccatctggct 1319
 |||||
 Db 1273 atggtgctgcccagagtcgaagctggctctctggtatgatgacccaccatctggct 1332
 QY 1320 aaagatctgggggtctctctctctataagggtcactctagcacagaggctgagtcac 1379
 |||||
 Db 1333 aaagatctgggggtctctctctctataagggtcactctagcacagaggctgagtcac 1392
 QY 1380 gggaaagagtcacactcctgacctagtcactctgccccaccactctcttactgtggaa 1439
 |||||
 Db 1393 gggaaagagtcacactcctgacctagtcactctgccccaccactctcttactgtggaa 1452
 QY 1440 aaccatctcagtaagaacctaaagtgtccagagacagagaagagaaggaagtgatctgg 1499
 |||||
 Db 1453 aaccatctcagtaagaacctaaagtgtccagagacagagaagagaaggaagtgatctgg 1512
 QY 1500 aattggagagagcctccaccaccctgactcctctatgaagccagctgtaaatla 1559
 |||||
 Db 1513 aattggagagagcctccaccaccctgactcctctatgaagccagctgtaaatla 1572
 QY 1560 gctactcaccaagagtgaggggagagagactccagtcactgagtcctccaggcccttg 1619
 |||||
 Db 1573 gctactcaccaagagtgaggggagagagactccagtcactgagtcctccaggcccttg 1632
 QY 1620 atctgtaccccccactatcttaaccaccacttgctccactccagctccctgtattga 1679
 |||||
 Db 1633 atctgtaccccccactatcttaaccaccacttgctccactccagctccctgtattga 1692
 QY 1680 tataacctgtcaggtcgtggttaggtttactgaggcagagagatagggaatcctta 1739
 |||||
 Db 1693 tataacctgtcaggtcgtggttaggtttactgaggcagagagatagggaatcctta 1752
 QY 1740 ttaaacataacatgaatatgtgtgttttctcattgtcgaatttaaatgaatacacaat 1799
 |||||
 Db 1753 ttaaacataacatgaatatgtgtgttttctcattgtcgaatttaaatgaatacacaat 1812
 QY 1800 gtttgtatgaaaaa 1813
 |||||
 Db 1813 gtttgtatgaaaaa 1826
 |||||
 RESULT 13
 AAZ65278
 ID AAZ65278 standard; DNA; 1932 BP.
 AC AAZ65278;
 XX 23-MAR-2000 (first entry)
 DT
 XX
 DE Human secreted protein gene 29.
 XX
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;

KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PD 18-NOV-1999.
 XX
 PN WO958660-A1.
 PF 06-MAY-1999; 99WO-US09847.
 XX
 PR 12-MAY-1998; 98US-0085093.
 PR 12-MAY-1998; 98US-0085094.
 PR 12-MAY-1998; 98US-0085105.
 PR 12-MAY-1998; 98US-0085180.
 PR 18-MAY-1998; 98US-0085906.
 PR 18-MAY-1998; 98US-0085920.
 PR 18-MAY-1998; 98US-0085921.
 PR 18-MAY-1998; 98US-0085922.
 PR 18-MAY-1998; 98US-0085923.
 PR 18-MAY-1998; 98US-0085924.
 PR 18-MAY-1998; 98US-0085928.
 PR 18-MAY-1998; 98US-0085925.
 PR 18-MAY-1998; 98US-0085927.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
 PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;
 PI Lafleur DW, Endress GA, Ebner R;
 PI
 XX
 DR WPI; 2000-062296/05.
 DR P-PSDB; AAY76152.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders -
 XX
 PS Claim 1; Page 313-314; 475pp; English.
 XX
 CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
 CC AAY76124 to AAY76223 represent the secreted proteins encoded by the 97
 CC human genes. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions,
 CC e.g. by protein or gene therapy. Also pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new genes. Specific
 CC uses are described for each of the 97 genes, based on which tissues they
 CC are most highly expressed in, and include developing products for the
 CC diagnosis or treatment of cancer, tumours, developmental abnormalities
 CC and foetal deficiencies, blood disorders, diseases of the immune system,
 CC autoimmune diseases, inflammation, allergies, asthma, psoriasis and cognitive
 CC disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin
 CC disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
 CC disorders, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners.

SQ Sequence 1932 BP; 405 A; 585 C; 514 G; 424 T; 4 other;

| | | | | |
|-----------------------|--------------|---------------|------------|--------------|
| Query Match | 98.4%; | Score 1783.8; | DB 21; | Length 1932; |
| Best Local Similarity | 99.7%; | Pred. No. 0; | | |
| Matches 1804; | Conservative | 3; | Mismatches | 1; |
| | | | Indels | 2; |
| | | | Gaps | 2; |

Dy 4 gccgcacctgggtgtagcagcgctccgcgcacgctccgcccgtcgcagcctcgg 63
|||||
Db 9 gccgcacctgggtgtagcagcgctccgcgcacgctccgcccgtcgcagca-actcgg 67

Qy 64 caactcgcaggtcctgcgtgcccgcggtgcgccctgactcgtgcccgccagggaggg 123
|||||
Db 68 caactcgcaggtcctgcgtgcccgcggtgcgccctgactcgtgcccgccagggaggg 127

QY 124 ccatgattccctccggggcccccgtgacccaactgctgcggttttgttctctgggc 183
|||||
D6 128 ccatgattccctccggggcccccgtgacccaactgctgcggttttgttctctgggc 187

QY 184 tgaatgcacctgcgccccctcgcgggcccagactgcaactgtccacttgcgcgccaacgcgt 243
|||||
Dh 188 tgaatgcacctgcgccccctcgcgggcccagactgcaactgtccacttgcgcgccaacgcgt 247
|||||

QY 244 tgcagcgcgctgagggagggagtgctctccagcgctgacacctgcacggggag 303

Db 248 tgcagcgcgctgagggagggagtgctctccagcgctgacacctgcacggggag 307

304 cgcttccatccagcagcagtcgcccctctgtgagtcgtctccaacagaaagaa 363
 |||||
 308 cgcttccatccagcagcagtcgcccctctgtgagtcgtctccaacagaaagaa 367

364 aggaagatcaggtgtgtcctcacatcaatgggggtccacaacaagcaaacctggatcct 423
 |||||
 368 aggaagatcaggtgtgtcctcacatcaatgggggtccacaacaagcaaacctggatcct 427

Db 428 tggctctactccatgcccctcccggaacctgtccctgcgctggaagggtctccagagaagaag 487

488 actctgcacctacagctgtccctcgtgatctgcaagaacaacaaagcgaatctagggcc 547

Db 548 acagatcaaaacccatgaactcaatgtagcttctctccagctcctccatcctgacctc 607

Db 608 tccagggtgtgtcccccattgtgtggggcacaagtgcacccttgagctgtccagtcctccaaggagta 667

Db 668 agccgcgtcacaataacagcgggacgcgcagctccatccctccagactctcttgcac 727

| Qy | 724 | cgagcatcagatgcacgcgtgggtcctctaagcctccacaaaccttcgtcttccatggtc | 783 |
|----|-----|---|-----|
| | | | |
| Db | 728 | cgagcatcagatgcacgcgtgggtcctctaagcctccacaaaccttcgtcttccatggtc <td>787</td> | 787 |
| Qy | 784 | gagtcatagtctgcgaagccccaacatcagagtggtggcactgcccacatgtaatgtaacgtcg | 843 |

Db 788 gggctctatgtctgcagaagccccaatgaggtggtgcactg--ccaatgtaatgtatgcagctgg 846

QY 844 aagtgagagcaacagggcctcgcagctgcagatggttcctcgcagagctgtctgttgggtatccctcgttcg 903

D0 847 aaatcagacacagggcctcgagctcagctggtctgctgagctgtctgtggtatccctgtctg 906

D1 904 gaactggggctgctgctgctgctgctgctcctctgtacacacagcaggggcaagggcctctgagag 963

Db 907 gaactgggtgtcgtgctgctgtctctctgtaccacgcgcgggcaaggccctggagg 966

Qy 964 agccagccaatgatattcaaggagatgccattgtccccggagaccctgtccctggcccaaga 1022

Db 967 agcagagccaatgatatcacaaggagatgccaattgtcccccggaacctgtccttgcccccaaga 1026

QY 1024 gctcagacacaatctccaagatgggaaccttctctctgtcaccttcgacagagaccttc 1083

Db 1027 gctcagacacatctccaagatgggaccccttcctctgcaaccctccagagccctcc 1086

Qy 1084 ggacacccatggccctccacgagctggtgatgacccacgcccagctctccagcc 1143

DB 1087 ggcaccccatggccctcccaaggcctgtgtgatctgaccccccaagccagctctctccagcc 1146

OY 1144 aggcctgtccctcaccaagactgcccacgacagatgggggccacccctcaaccaatatccc 1203

DB 114 / agggccctctgcctccctccacgaagacatgcgccacgacagatgaggggcccaaccctccaaacaaatcccc 1206

QY 1204 ccacatccctggtgagggttctctccctctggtccttgagccgcaatggtgctgtgctctgtgatgg 1263

1264 tgcctgcaccagatgcaggctcgtctctcgtgatgagaccaccacatctggtctaaag 1323

DN 4267 TGCCTGAGGGATCAGTCCCGTTTCACCTGTAAATGGAAGAATTGATGCTAAGGCAAGTGCTGTA
QY 1324 GATTGCGGTCTCTCCTCTCATATAAGGTGTCACCTCTAGACAAGAGGCCCTGAGTCAATGGGA

202 5aaagatcacaactcctgaaccccttaftactctgcccccaacctctcttactgctgggaaacc 1443

1444 atctcagtaagcctaagtctccaggagacagaaaggaggaagtggatctcgaattc 1503

1504 gggaggagcctccaccacccctgactcctctatgaagcagctgctgaattagcta 1563

QY 1564 ctccaagagtgaggggcagaacttccagtcactgagtcctccagccccctgacatc 1623

Db 1567 ctccaccaagatgaggggcagagacttccagtcagtcagtcctccagggcccttgatct 1626
Qy 1624 gtaccaccacctatataaccacccttggctcccaactcagctccctgtattgata 1683
Db 1627 gtaccaccacctatataaccacccttggctcccaactcagctccctgtattgata 1686
Qy 1684 acctgtcagctgtctgtgttgatttactctggggcagagatagggaatctctat 1743
Db 1687 acctgtcagctgtctgtgttgatttactctggggcagagatagggaatctctat 1746
Qy 1744 aactaacatgaatatgtgtgtttcatttgcgaatttaataagaatacataatgtt 1803
Db 1747 aactaacatgaatatgtgtgtttcatttgcgaatttaataagaatacataatgtt 1806
Qy 1804 gtatgaaaaa 1813
Db 1807 gtatgaaaaa 1816

RESULT 14
AAC85076
ID AAC85076 standard; DNA; 1831 BP.
XX
AC AAC85076;
XX
DT 08-MAY-2001 (first entry)
XX
DE Atherosclerosis-associated gene seq ID No. 12.
XX
KW Atherosclerosis-associated gene; stroke; myocardial infarction; human;
KW ischemia; coronary artery disease; angina pectoris; hypertension;
KW peripheral vascular disease; renal artery stenosis; atherosclerotic;
KW cerebroprotective; cardiact; gene therapy; hypotensive; vasotropic;
KW antianginal; ds.
XX
OS Homo sapiens.
XX
PN WO200104264-A2.
XX
PD 18-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-US17887.
XX
PR 07-JUL-1999; 99US-0349015.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Jones KA, Volkmuth W, Walker MG;
XX
DR WPI; 2001-138330/14.
XX
PT Composition comprising atherosclerosis-associated polynucleotide useful
PT in diagnosis, prognosis, treatment, and prevention of atherosclerosis
PT and stroke, myocardial infarction, or hypertension -
XX
PS Claim 1; Page 43; 58pp; English.
XX
CC The invention provides novel atherosclerosis-associated polynucleotides

CC and polypeptides encoded by the genes. Expression vectors and host cells
CC for producing the polypeptides are disclosed and methods for screening
or
CC purifying ligands which specifically bind to the polypeptides are also
CC provided. The polynucleotides are useful for treating diseases
associated
CC with the altered expression of a gene that is coexpressed with one or
CC more known atherosclerosis-associated genes in a subject. They are
CC useful in diagnosis, prognosis, treatment, prevention, selection and
CC evaluation of therapies for atherosclerosis including stroke, myocardial
CC infarction, transient cerebral ischemia, mesenteric ischemia, coronary
CC artery disease, angina pectoris, peripheral vascular disease, renal
CC artery stenosis, and hypertension. Sequences AAC85065-85098 represent
CC atherosclerosis-associated genes of the invention.
XX
SQ Sequence 1831 BP, 370 A; 561 C; 494 G; 406 T; 0 other;

Query Match 97.1%; Score 1760.4; DB 22; Length 1831;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1807; Conservative 0; Mismatches 6; Indels 13; Gaps 3;

Qy 1 ggaagccgccttgggtgtcagcggctcggtccgcgcagctccggccgtcgcgagcct 60
Db 3 ggaagccgccttgggtgtcagcggctcggtccgcgcagctccggccgtcgcgacctc 62
Qy 61 cggcacctgcaggtccgt-gcgtcccgcggt-ggcgcacctgactccgtccgcgcagg 118
Db 63 gggcacctgcaggtccgtcccgcggtccgcgcagctccgcgcacctgactccgcgcagg 122
Qy 119 gagggcacatgattccctcccggggccccctggtgaccacattgctcggttttgttcc 178
Db 123 gagggcacatgattccctcccggggccccctggtgaccacattgctcggttttgttcc 182
Qy 179 ggggtcgtagtcctccgc 238
Db 183 ggggtcgtagtcctccgc 242
Qy 239 ccggttcaggccggtggaaggagggaagtgtgtccagcgtgtacaccttgacagg 298
Db 243 ccggttcaggccggtggaaggagggaagtgtgtccagcgtgtacaccttgacagg 302
Qy 299 ggaagtgtctcatccagccatgggaagtgcccttgtgatgtgttcttcaaacagaa 358
Db 303 ggaagtgtctcatccagccatgggaagtgcccttgtgatgtgttcttcaaacagaa 362
Qy 359 agaaaggagatcaggtgtgtcctacatcaatgggggtcacaacaaggaaacctggagt 418
Db 363 agaaaggagatcaggtgtgtcctacatcaatgggggtcacaacaaggaaacctggagt 422
Qy 419 atcctgttactactccatgcctcccggaacctgtccctgcggtggaaggtctccagga 478
Db 423 atcctgttactactccatgcctcccggaacctgtccctgcggtggaaggtctccagga 482
Qy 479 gaaagacttggccctacagctgtccgtgaatgtgcaagaacaagaaggcaaatctag 538
Db 483 gaaagacttggccctacagctgtccgtgaatgtgcaagaacaagaaggcaaatctag 542

QY 539 gggccacagcatcaaaaacctagaactcaatgtactggttctccagctcctccatcctg 598
|||||
Db 543 gggccacagcatcaaaaacctagaactcaatgtactggttctccagctcctccatcctg 602
599 ccgtctccagggtgtgtcccatgttg9gggcaaacgtgacctgaagctgcaggtctccaag 658
|||||
Db 603 ccgtctccagggtgtgtcccatgttg9gggcaaacgtgacctgaagctgcaggtctccaag 662
659 gagtaagcccgctgtctccaataccaagtgggatacgcgacagcttccatccttccagacttctt 718
|||||
Db 663 gagtaagcccgctgtctccaataccaagtgggatacgcgacagcttccatccttccagacttctt 722
QY 719 tgcacacagcatatagatgtcatccgtgggtctttaagcctcaaccaacttctgcttccat 778
|||||
Db 723 tgcacacagcatatagatgtcatccgtgggtctttaagcctcaaccaacttctgcttccat 782
QY 779 ggcctgagtcctatgtctgcaaggcccaacaatgaggtgggcaatgcccacatgtatgtgac 838
|||||
Db 783 ggcctgagtcctatgtctgcaaggcccaacaatgaggtgggcaatgcccacatgtatgtgac 842
QY 839 gctggaagtgaagcaaca-----gggcctggaagctgcagtggtgtgctggaagctgtt 887
|||||
Db 843 gctggaagtgaagcaacaggtcagtagaggggctggaagctgcagtggtgtgctggaagctgtt 902
QY 888 gtgggtacccctggttgagctgggtgtgctggctgggtcgtgcctctgtaccacgcgcgg 947
|||||
Db 903 gtgggtacccctggttgagctgggtgtgctggctgggtcgtgcctctgtaccacgcgcgg 962
QY 948 ggcaaggccctgggaaggagcccgccaatgataccaaggagagtgccaatgtctcccgagcc 1007
|||||
Db 963 ggcaaggccctgggaaggagcccgccaatgataccaaggagagtgccaatgtctcccgagcc 1022
QY 1008 ctgacctggcccaagagctcagacacaatctccaagaatgggaccttctctgtcaccc 1067
|||||
Db 1023 ctgacctggcccaagagctcagacacaatctccaagaatgggaccttctctgtcaccc 1082
QY 1068 tccgcagagagccctccggccaaccccatgacctcccgagctgtgtgcatgtgaccccccag 1127
|||||
Db 1083 tccgcagagagccctccggccaaccccatgacctcccgagctgtgtgcatgtgaccccccag 1142
QY 1128 cccagctctccagcagaagccctgacctcaaccaagaactgcccacagatggggccac 1187
|||||
Db 1143 cccagctctccagcagaagccctgacctcaaccaagaactgcccacagatggggccac 1202
QY 1188 cctcaaccaatatcccccatccctgtgggttctctcctctgacctgaagccgcatgggt 1247
|||||
Db 1203 cctcaaccaatatcccccatccctgtgggttctctcctctgacctgaagccgcatgggt 1262
QY 1248 gctgtgctgtgtgtgtgctgtccagagtcgaagctggtctctgttatatgaacccac 1307
|||||
Db 1263 gctgtgctgtgtgtgtgctgtccagagtcgaagctggtctctgttatatgaacccac 1322
QY 1308 cactcatgtgctaaaggatltggggtctctcctctctataaagggtcacctctagcacaga 1367
|||||
Db 1323 cactcatgtgctaaaggatltggggtctctcctctctataaagggtcacctctagcacaga 1382
QY 1368 ggcctgagtcatgggaaagagtcacactcctgaccttagtactgtgccccacactctct 1427
|||||

Db 1383 ggcctgagtcatgggaaagagtcacactcctgaccttagtactgtgccccacactctct 1442
QY 1428 ttactgtgggaaaaacacatctcagtaagacctaaagtgtccaaggagacagaaggagaagg 1487
|||||
Db 1443 ttactgtgggaaaaacacatctcagtaagacctaaagtgtccaaggagacagaaggagaagg 1502
QY 1488 aagtgtatctggaatgtgggaaggacctccaccaccacctgactcctccttatgaagccag 1547
|||||
Db 1503 aagtgtatctggaatgtgggaaggacctccaccaccacctgactcctccttatgaagccag 1562
QY 1548 ctgctgtaaatagctactcacccaagagttaggggcagagacttccagtcactgagtctcc 1607
|||||
Db 1563 ctgctgtaaatagctactcacccaagagttaggggcagagacttccagtcactgagtctcc 1622
QY 1608 caggcccccttgatctgtacccccaccctatcaacaaccaaccttggtcctccactccagc 1667
|||||
Db 1623 caggcccccttgatctgtacccccaccctatcaacaaccaaccttggtcctccactccagc 1682
QY 1668 tccctgtatctatataacctctcagagctggcttggttaggtttactggggcagagata 1727
|||||
Db 1683 tccctgtatctatataacctctcagagctggcttggttaggtttactggggcagagata 1742
QY 1728 gggaaatctctatataaacaacatgaatatgtgtgtttcatcttgcaatttaata 1787
|||||
Db 1743 gggaaatctctatataaacaacatgaatatgtgtgtttcatcttgcaatttaata 1802
QY 1788 aagatacataatgttctgtatgaaaaa 1813
|||||
Db 1803 aagatacataatgttctgtatgagata 1828

RESULT 15

AAFA4978
ID AAFA4978 standard; cDNA; 1869 BP.

XX AAFA4978;

XX 28-MAR-2001 (first entry)

XX Human INTERCEPT 258 coding sequence SEQ ID NO: 26.

XX Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;

KW INTERCEPT 258; coronary disorder; olfactory disorder;

KW neurological disorder; pulmonary disorder; immunological disorder;

KW developmental disorder; kidney disorder; ss.

OS Homo sapiens.

XX WO200078808-A1.

XX 28-DEC-2000.

XX 19-JUN-2000; 2000WO-US16883.

XX 18-JUN-1999; 99US-0336536.

XX (MILL-) MILLENNIUM PHARM INC.

PI Leiby KR, McKay C, Bosson S;
XX
DR WPI; 2001-050109/06.
XX
PT New nucleic acids for treating diseases and disorders, e.g.
PT atherosclerosis, infection, autoimmune diseases, obesity, ear
PT disorders, brain disorders, tumors, diabetes, arthritis, multiple
PT sclerosis and asthma -
XX
PS Claim 1; Page 227; 332pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human and murine secreted or transmembrane proteins TANGO 253, TANGO
257,
CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of
CC coronary, pulmonary, olfactory, immunological, neurological,
CC developmental and kidney disorders.
XX
SQ Sequence 1869 BP; 391 A; 568 C; 496 G; 408 T; 6 other;

Query Match 96.9%; Score 1757.6; DB 22; Length 1869;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 22; Indels 2; Gaps
2;

QY 1 ggagccgcccgtgtgtcagcggtcgcgtcccgcgacgctccggcgcgtgcgacgct 60
DB 28 ggagccgcccgtgtgtcagcggtcgcgtcccgcgacgctccggcgcgtgcgacgct 87

QY 61 cggcacctgcaggtccgtgcgtcccgcggtgcgccttgaactccgtcccgccaggga 120
DB 88 cggcacctgcaggtccgtgcgtcccgcggtgcgccttgaactccgtcccgccaggga 147

QY 121 gggccatgattccctccgggggccccctgtgtgacaaactgtgcggtttttgtcctgg 180
DB 148 gggccatgattccctccgggggccccctgtgtgacaaactgtgtcgtttttgtcctgg 207

QY 181 ggctgaagtccctcgcgccccctcgcgggccacgtgcaactgcaactgcccgcacaac 240
DB 208 ggctgaagtccctcgcgccccctcgcgggccacgtgcaactgcaactgcccgcacaac 267

QY 241 ggttcagcgcggtggagggaagggaagtgtgtctccagcggtgtacacctgtgacgggg 300
DB 268 ggttcagcgcggtggagggaagggaagtgtgtctccagcggtgtacacctgtgacgggg 327

QY 301 aggtgtctcatcccaagcatgggaggtgtcccttgtgattgtgttcttcaaacagaaag 360
DB 328 aggtgtctcatcccaagcatgggaggtgtcccttgtgattgtgttcttcaaacagaaag 387

QY 361 aaaaggagagatcaggtgtgtctcatcatcaatggggtcacaaagaacaaacttgagtat 420
DB 388 aaaaggagagatcaggtgtgtctcatcatcaatggggtcacaaagaacaaacttgagtat 447

QY 421 ccttggtctactccatcgccctccggaacctgtccctgcggtggaagggtctccagagaga 480
DB 448 ccttggtctactccatcgccctccggaacctgtccctgcggtggaagggtctccagagaga 507

QY 481 aagacttggccccctaaagctgtctccgtgaatgtgcagaacaaaggcaatctcagg 540
DB 508 aagacttggccccctaaagctgtctccgtgaatgtgcagaacaaaggcaatctcagg 567

QY 541 gccacagcatcaaaacctagaactcaatgtactgttctccagctccctccatccctggc 600
DB 568 gccacagcatcaaaacctagaactcaatgtactgttctccagctccctccatccctggc 627

QY 601 gtctccaggtgtgcccccatgtggyggggcaaacgtgacacctgtagctgcacgtctccaagga 660
DB 628 gtctccaggtgtgcccccatgtggyggggcaaacgtgacacctgtagctgcacgtctccaagga 687

QY 661 gtaagcccgctgtccaataccagtgaggatcggcagcttccatccctccagacttcttg 720
DB 688 gtaagcccgctgtccaataccagtgaggatcggcagcttccatccctccagacttcttg 747

QY 721 caccagcatatgattgtcatccgtggtgtcttaagccctcaccaaccttctgtcttccatgg 780
DB 748 caccagcatatgattgtcatccgtggtgtcttaagccctcaccaaccttctgtcttccatgg 807

QY 781 ctggaagtctatgtctgcaagggcccaaatgagtgggcactgcccgaatgtaatgtgacgc 840
DB 808 ctggaagtctatgtctgcaagggcccaaatgagtgggcactgcccgaatgtaatgtgacgc 867

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DB 868 tggaaagtgcacaggggcttgtagctgagtcgtgtgtcgtgagctgtgtgtggtraccctgg 927

QY 901 ttggactgggggttgcgtggtgtggtgtctctcttgtaccaccggcggggcaaggccctgg 960
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 Job time: 4314 sec

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:02:47 ; Search time 54.72 Seconds
(without alignments)
8138.405 Million cell updates/sec

Title: US-09-902-759-38
Perfect score: 1813
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

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- 6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 45.4 | 2.5 | 1584 | 4 | US-08-928-383B-1 |
| 4 | 45.4 | 2.5 | 2434 | 4 | US-09-272-496-1 |
| 5 | 44.2 | 2.4 | 4403765 | 4 | US-09-103-840A-2 |
| 6 | 43.4 | 2.4 | 4403765 | 4 | US-09-103-840A-2 |
| 7 | 42.4 | 2.3 | 1095 | 4 | US-08-928-383B-3 |
| 8 | 42.2 | 2.3 | 2830 | 1 | US-07-882-292-1 |
| 9 | 42.2 | 2.3 | 2830 | 2 | US-08-331-644-1 |
| 10 | 42.2 | 2.3 | 2830 | 5 | PCT-US93-04102-1 |
| 11 | 41.8 | 2.3 | 477 | 4 | US-09-135-994-1 |
| 12 | 41.6 | 2.3 | 1515 | 4 | US-08-928-383B-25 |

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| C 26 | 37.8 | 2.1 | 2655 | 2 | US-08-471-044-26 | Sequence 26, Appli |
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| C 29 | 37.8 | 2.1 | 2655 | 2 | US-08-471-046A-17 | Sequence 17, Appli |
| C 30 | 37.8 | 2.1 | 2655 | 2 | US-08-471-046A-26 | Sequence 26, Appli |
| C 31 | 37.8 | 2.1 | 2655 | 2 | US-08-470-566B-17 | Sequence 17, Appli |
| C 32 | 37.8 | 2.1 | 2655 | 2 | US-08-470-566B-26 | Sequence 26, Appli |
| C 33 | 37.8 | 2.1 | 2655 | 2 | US-08-469-334-17 | Sequence 17, Appli |
| C 34 | 37.8 | 2.1 | 2655 | 2 | US-08-469-334-26 | Sequence 26, Appli |
| C 35 | 37.8 | 2.1 | 2655 | 3 | US-09-300-529-17 | Sequence 17, Appli |
| C 36 | 37.8 | 2.1 | 2655 | 3 | US-09-300-529-26 | Sequence 26, Appli |
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| C 38 | 37.8 | 2.1 | 4031 | 2 | US-08-471-044-49 | Sequence 49, Appli |
| C 39 | 37.8 | 2.1 | 4031 | 2 | US-08-463-483A-49 | Sequence 49, Appli |
| C 40 | 37.8 | 2.1 | 4031 | 2 | US-08-470-566B-49 | Sequence 49, Appli |
| C 41 | 37.8 | 2.1 | 4031 | 2 | US-08-469-334-49 | Sequence 49, Appli |
| C 42 | 37.8 | 2.1 | 4031 | 2 | US-08-470-566B-49 | Sequence 49, Appli |
| C 43 | 37.8 | 2.1 | 4031 | 3 | US-09-300-529-49 | Sequence 49, Appli |
| C 44 | 37.4 | 2.1 | 320 | 4 | US-09-165-264-7 | Sequence 7, Appli |
| C 45 | 37 | 2.0 | 1682 | 4 | US-09-318-443-7 | Sequence 7, Appli |

ALIGNMENTS

RESULT 1
US-08-979-424-2
; Sequence 2, Application US/08979424
; Patent No. 5942606
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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: SOFTWARE: FastSeq for Windows Version 2.0
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/979,424
: FILING DATE: Filed Herewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0405 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-855-0555
: TELEFAX: 650-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1387 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: LUNGRET03
: CLONE: 1232054
: US-08-979-424-2

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US-08-232-463-14

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Matches 10; Conservative 219; Mismatches 150; Indels 0; Gaps
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:00:57 ; Search time 1589.67 Seconds
(without alignments)
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Perfect score: 1813

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Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| C 7 | 942 | 52.0 | 955 | 9 | AL571713 | AL571713 |
| C 8 | 937.2 | 51.7 | 1026 | 9 | AL573957 | AL573957 |
| 9 | 911.6 | 50.3 | 969 | 9 | AL548482 | AL548482 |
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| C 11 | 910.2 | 50.2 | 998 | 9 | AL572321 | AL572321 |
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| 18 | 886.2 | 48.9 | 920 | 9 | AL553280 | AL553280 |
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| 31 | 777 | 42.9 | 885 | 10 | BI767362 | BI767362 |
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ALIGNMENTS

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 VERSION AL573851.1 GI:12933489
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1069)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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 /clone="CSOD1054Y101"
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 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
 BASE COUNT 248 a 269 c 327 g 224 t 1 others
 ORIGIN

Query Match 56.6%; Score 1026.2; DB 9; Length 1069;
 Best Local Similarity 99.5%; Pred. No. 2.7e-232;
 Matches 1050; Conservative 0; Mismatches 3; Indels 2; Gaps

QY 714 ttctttgaccagcattagatgcatcgcgtgggtctttaagcctcaaccatttcgtct 773
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 Db 1061 TTCTTGCACCAAGCATTAATGATGTCATCCGTGGGCTTTTAAGCCTCAACCACTTTGCTCT 1002
 QY 774 tccatggctgagatcattgtctgcaagcccaacaatgagtgaggcaatgcccaatgtaat 833

Db 1001 TCCATGGCTGGAGTCTATGTCTGCAGAGGCCCAATGAGGT -GGACTGCCCCAATGTAAT 943
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 Db 942 GTGACGCTGGAAGTGAACACAGAGGCGCTTGAGCTGAGTGTCTGAGACTGTTGTGGGT 883
 QY 894 accctggttggaactgggggttgctgctgctgctgctctgttaccacgcccggggcaag 953
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 Db 882 ACCCTGGTGTGACTGGGGTGTGCTGGGCTGTGCTCTTGTACACACGCGGGGCAAG 823
 QY 954 gccctggaagagccagcgaatgatatacaaggagatgcatctgtcccccgaacctgccc 1013
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 Db 822 GCCCTGAGAGAGCAGCCAGCAATATATCAAGAGGATGCCATTGCTCCCGGAGCCCTGCCC 763
 QY 1014 tggcccaagagctcagacacaactcctcaagaatgggaccccttctctgtcactccgca 1073
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 Db 762 TGCCCAAGAGCTCAGACACAATCTCAAGATGGAGCCCTTCTGTCTGTCACCTCGCA 703
 QY 1074 cgagccctcgagccaccaccatggtccctccagagcctgtgcatgtgaccccaagccagct 1133
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 Db 702 CGAG -CCTCCGGCCACCCCATGAGCCCTCCAGAGCCTGTGATGACCCCAAGCCAGT 644
 QY 1134 ctctccagccaggccctgcccctcaacaaagactgcccagacagatggggcccacccctcaa 1193
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 Db 643 CTCTCCAGCCAGGCCCTGCGCTCCTCAAGACTGCCACGACAGATGGGGCCACCCCTCAA 584
 QY 1194 ccaatacccccatccctggtgggttcttctctggtctgagccgcatgggtcgtgtg 1253
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 Db 583 CCAATATCCCCCATCCTGTGTGGGTTTCTTCTCTGTGCTGAGCCGATGGGTGTGTGTG 524
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 Db 523 CCTGTGATGTGTCCTGCCCAAGTCAAGCTGGCTCTGTGTATGATGACCCCACTCTCA 464
 QY 1314 ttggtctaaagattgggggtctctctctctataaaggtcacctctgacacagagcctg 1373
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 Db 463 TTGGCTAAAGATTGGGGTCTCTCTCTTAAGGGTCACTCTTGACACAGAGGCGCTG 404
 QY 1374 agtcattgggaagagtcacacatcctgaccccttagtactctgcccccaactctcttactg 1433
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 Db 223 AAATTAGCTACTCACCAAGAGTGAAGGGGCAAGACTTCCAGTCACTAGTCTCCAGGCC 164
 QY 1614 cccttcatctgtaaccccaacctatctaacacacacctgtgctcccaactccagctccctg 1673
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 Db 163 CCCTTGAATCTGTACCCACCCCTATATTAACACACCCTTGGCTCCCACTCCAGCTCCTG 104

QY 1674 tattgataaacctgcagctgcttggttaggtttactcgggcagagatagggaat 1733
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Db 103 TATTGATATAACCTGTAGGCTGCTGTGTTAGTTACTGGGCGAGAGATAGGGAAT 44
QY 1734 cctctaataaactaacatgaatatgtgtctt 1768
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Db 43 CTCTTATTAATACTAATGATATGTGTGTTT 9

RESULT 2
AL547358 AL547358 1017 bp mRNA linear EST
LOCUS 16-FEB-2001
DEFINITION AL547358 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI007YN05 5
prime, mRNA sequence.

ACCESSION AL547358
VERSION AL547358.1 GI:12881364
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1017)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source 1.1017
/organism="Homo sapiens"
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/clone="CSODI007YN05"
/clone_lib="LTI_NFL006_PL2"
/issue_type="placenta"
/note="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 185 a 311 c 305 g 215 t 1 others
ORIGIN

Query Match 55.5%; Score 1005.6; DB 9; Length 1017;
Best local Similarity 99.8%; Pred. No. 2e-227;
Matches 1016; Conservative 1; Mismatches 0; Indels 1; Gaps

QY 13 ggtgtcagcgctcggtcccgcgcaagctccgcgcgctgcgcagcctcgacatgcag 72
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Db 1 GGTGTCAAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGGCGAG-CTCGGCACCTGCAG 59
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Db 60 GTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCGCCGCGCAGGAGGCGCATGATTT 119
QY 133 cccctccgggggccccctggtgaaccaactgtcgtcggttttgttcctcgggggtcgaagtc 192
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Db 120 CCTCCCGGGGGCCCCCTGTGACCAACTTGTGCGGTTTGTTCCTGGGGCTGAGTGC 179

QY 193 tcgccccccctcgcgggcccaagtcgaactgcactgcccgcgaacgggtgcagcg 252
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Db 180 TCGCGCCCCCTCGCGGGCCCAAGTCGACACTTGCCTCCGCCCAACGGTTCGAGCGG 239

QY 253 tggaggaggggaagtggtgtctccagcgtggtacacctgtcacggggaggtgtctcat 312
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Db 240 TGGAGGAGGAGGGAAGTGTGTCTCCACGCTGTGACACTTGACGCGGAGGTCTTCAT 299

QY 313 cccagccatgggaagtggtcccttgtgatgtgtcttcaacagaagaagaagagatc 372
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Db 300 CCCAGCCATGGGAGGTGCCCTTTGTGATGTGTTCTTCAACAGAAAGAGAGATC 359

QY 373 aggtgtgtcctacatcaatgggttcacaacaaagcaaacctggagtaacctgtgtact 432
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Db 360 AGGTGTGTCTCATCATCATGAGGGTCAACAAGCAAACTGGAGTATCTTGTGTACT 419

QY 433 ccattgccccccggaacctgtccctggtcggtggaaggtctccaggagaaagatctgtgc 492
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Db 420 CCATGCCCTCCCGGAACCTGTCCCTGCGGTGAGGAGTCTCCAGAGAAAGACTCTGCCC 479

QY 493 cctacagctgtccgtgaatgtgcaagacaacaaagcaaatctaggggccacagatca 552
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Db 480 CCTACAGCTGTCCGTGATGTGCAGAACAAAGCAAACTTAGGGGCCACAGATCA 539

QY 553 aaacctagaactcaatgtactggttcctccagctcctccatcctgcgcgtccagggtg 612
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Db 540 AAACCTTAGAATCAATGATGACTGTTCTCCAGCTCCTCCATCTGCCGTCTCCAGGGTG 599

QY 613 tggcccatgtgggggcaaacgtgacctgagctgccaagtcctcaaggagtaagccggtg 672
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Db 600 TGCCCCATGTGGGGCAACGTGACCTGAGCTGCCAGTCTCCAGAGTAAGCCCGCTG 659

QY 673 tccaatccagtggaatcgcgagcttccatcctccagacttcttgcaccagcatag 732
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Db 720 ATGTCAATCGTGGGTCTTTAAGCTCACCAACTTGTGTTCATGAGCTGAGTCTATG 779

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 Db 900 TGCTGGCTGGGCTGTCCTTTGTACACCGCCGGGGCAAGCCCTTGAGAGACCCAGCCA 959
 Qy 973 atgatacaagaagatgcatctgtcccccggaccctgtccctgtgcccagaagctcaga 1030
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 Db 960 ATGATATCAAGAGAGATGCAATGTGCTCCCGGACCTGCGCTGGSCCAAGACTCAGA 1017

RESULT 3
 AL513572 1045 bp mRNA linear EST
 LOCUS 13-FEB-2001
 DEFINITION AL513572 LTI_NFL006_PL2 Homo sapiens cDNA clone XCL0BA001ZD03 5
 prime, mRNA sequence.
 ACCESSION AL513572
 VERSION AL513572.1 GI:12777066
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1045)
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source 1..1045
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 /db_xref="taxon:9606"
 /clone="XCL0BA001ZD03"
 /clone_lib="LTI_NFL006_PL2"
 /issue_type="placenta"
 /note="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 196 a 304 c 302 g 229 t 14 others
 ORIGIN

Query Match 54.7%; Score 992.4; DB 9; Length 1045;
 Best Local Similarity 97.0%; Pred. No. 2,7e-224;
 Matches 1015; Conservative 14; Mismatches 15; Indels 2; Gaps

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 Qy 71 aggtccggtgcgtcccgcgctggtcgccctgaactccggtcccgccaggaggccatgat 130
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 Db 60 AGGTCCGTGCGTCCCGCGGTGGCGCCCTGTACTCCGTCGCCGCGCAGGAGGCCATGAT 119
 Qy 131 ttccctccgggggccccctggtgaccactgtgtcggtttttgttctctggggtgagtc 190
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 Db 120 TTCCCTCCCGGGGCCCTGTGTACCACTTGCTGCGGTTTTGTCTCTGGGCTGATGTC 179
 Qy 191 cctcgccccctcgcggtcccaagtgcactgtgacgtgcccgaaccggtgcagcc 250
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 Db 180 CCTCGGCCCCCTCGGGGCCAGTGCACATGCACTTGCCGCCAACCGGTTGCAGGC 239
 Qy 251 ggtggaagggaagatggtgtctccagcgtgtacactgtgacggggaaggtgtcttc 310
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 Db 240 GGTGAGAGGAGGGAAGTGTGTCTTCCAGCGGTGTACACTTGACAGGGGAGGTGTCTTC 299
 Qy 311 atcccaagcattggaaggtgcccccttgtgtgtgtcttcaacagaagaagaaggga 370
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 Db 300 ATCCACGCMATGGAGGTGCTCCCTTGTGATGTGTTCTTCAAMARAPARAAGAGAGA 359
 Qy 371 tcaggtgtgtcctacatacaatggtgtcacacaagaacacgtgagtatcctgtgtcta 430
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 Db 360 TCAGGTGTGTCTTACATCAATGAGGCTCACACAAGCAACTGTGAGTATCTTGCTTA 419
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 Db 420 CTCATGCTCTCCCGGAACCTGTTCTGCGGCTGAGGCTTCCAGAGAAARACTGTGG 479
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 Db 600 TGTGCCCATGTGGGGCCAAAGTGACCTGAGTCCAGTTTCCAAAGAGTWAAGCCGCG 659
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 Qy 731 agatgtcatcgtggtgtcttcaagcctcaccaacttctgttccatgctgtgagtccta 790
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 Db 720 AGATGTATCCGTGGGTTTAAAGCTTCACCAACTTTGCTTCCATGGCTGAGATTTA 779
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 Db 780 TGTTTGCAAGGCCACCAATGAGTGGGACCTGCCAATGTAAATGTGACGCTGGAAGTGA 839
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 Db 840 CACAGGCGCTGAGCTGCAGTTGTTGTGAGACTGTTGTGGGA-CCTGATTGAGACTGGG 898

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 Db 899 GTTGCTGCTGGCTGGCTGCTCTTGTATCCAMCGCCGGGGCAAGGCCCTTGAGAGGACGAC 958
 QY 971 caatgatatcaaggaggaatgcattgctccccgagacctgacctggtcccaagagctcaga 1030
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 Db 959 MATGAMATMAAGAGAGATGTCATTCTCCCGGACCCTGCGCTGGCCCAAGAGCTCAGA 1018
 QY 1031 cacaatctccaagaatgaggaccttt 1056
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 Db 1019 AAAAATYTCCAAGATTGGACCCCTT 1044

RESULT 4
 AL573030/c 986 bp mRNA linear EST
 LOCUS AL573030
 16-FEB-2001
 DEFINITION AL573030 LTI_NFL006_PL2 Homo sapiens cDNA clone CSOD1014YD08 3
 prime, mRNA sequence.
 ACCESSION AL573030
 VERSION AL573030.1 GI:12931874
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 986)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 212 a 250 c 302 g 210 t 12 others
 ORIGIN

Query Match 52.3%; Score 947.6; DB 9; Length 986;
 Best Local Similarity 98.1%; Pred. No. 1.le-213;
 Matches 969; Conservative 9; Mismatches 8; Indels 2; Gaps

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 QY 793 tctgcaaggcccaaatgagatggtggcaactgcccgaatgtaatgtgacgtggaagtgaaca 852
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 QY 853 cagggcctggagctgcagtggtgtgctggagctgtgtgtgtacctggttggactgggt 912
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 Db 927 CAGGGCCTTGAGAGCTGCACTGAGTGTGCTGAGAGCTGATGT-GGTACCTGTGTTGACTGGGGT 869
 QY 913 tgcctgctgggtggtgcctctgtaccacgcgcgggcaagggccctggaggagccagca 972
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 Db 868 GGCTGGCTGGGCTGCTGCTCTTGTATCCACCGCGGGGCAAGGCCCTGAGAGACCGACCA 809
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 Db 808 ATGATATCAAGGAGGATGCCATTGCTCCCCGGACCTTACCTTGCCCAAGAGCTCAGACA 749
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 Db 748 CAATCTCCAAGATGGGACCTTCTCTGTCACTCCGACAGAGCCCTCCGGCCACCC 689
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 Db 688 ATGGCCCTCCCAAGGCGCTGTGATTAACCCCAAGCCAGTCTCTCCAGCCAGGCCCTGC 629
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 Db 508 AGAGTCAAGCTGGCTCTGTGATGATGACCCCACTCCTGTTGCTTAAGGATTTGGGG 449
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 Db 388 ACTCCTAGCCCTTAGTACTGTGCCCCCACTCTCTTAATGTGGGAACCATCTCAGTA 329
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 Db 328 AGACTTAAGTGTCCAGGAGACAGAAAGAGAGAGTGTGATTGGAATTGGAGAGARC 269
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 Db 208 AGTGAGGGGCGAGAGACTTCCACTGAGTGTCTCCAGGCCCTTGATCTGTATCCCCAC 149

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 Db 28 GAAATATGTGTGTTTTCATATATGCAAAW 1
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 LOCUS 16-FEB-2001
 DEFINITION AL550211 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI039YD07 5
 prime, mRNA sequence.
 ACCESSION AL550211
 VERSION AL550211.1 GI:12886963
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1013)
 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
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 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 183 a 309 c 304 g 216 t 1 others
 ORIGIN

Query Match 52.3%; Score 947.6; DB 9; Length 1013;
 Best Local Similarity 99.3%; Pred. No. 1.1e-213;
 Matches 1003; Conservative 1; Mismatches 0; Indels 6; Gaps

5;
 QY 11 tgggtgtcaagcggcgtcggtcccgcgcaagctccggccgtcgcgcaagcctcggaactgc 70
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 Db 1 TGGGTGTCAAGCGGCTCGGCTCCCGCGACGCTCCGGCCGTGCGCGC--CCTCGGCACCTGC 58
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 QY 71 aggtccgtgctcccgcggtcggtcgccctcgaactccgtcccgccgaaggagggccatgat 130
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 Db 59 AGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCGGCCAGGAGGCCATGAT 118
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 QY 131 ttccctccgggggcccctgtgtaaccaactgtcggtcttctgtccttgaggctgagtc 190
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 Db 119 TTCCCTCCCGGGGCCCTGTGTACCACTTGCTGCGGTTTGTCTCGGGCTGAGTGC 178
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 QY 191 cctcgccccccctcgcggtccagctgcaactgcaactgcgcgcccaaccggtgcagcg 250
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 Db 179 CCTCGGCCCCCCTCGGGGGCCCAAGCTGCACTGCACTTGCCCCCAACGGTTGCGAGC 238
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 QY 251 ggtgagggaggggaagtgtgtctccagcgtgtgtacaccttgcaaggagggaggtgtcttc 310
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 Db 239 GGTGAGGAGGAGGGAAGTGTGCTTCCAGCGTGTAACCTTGACGGGGAGGTGTCTTC 298
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 QY 311 atcccgacatgggaagtgcccttctgtatgtgtcttcaacagaagaagaaggagga 370
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 Db 299 ATCCGAGCATGGAGGTGCCCTTGTGATGTGTTCTTCAACAGAAAGAGAGGA 358
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 QY 371 tcaggtgtgtcctacatcaatggtgtcacacaagaacaaactgtagtatcctgtgtcta 430
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 Db 359 TCAGGTGTGTCTTACATCATATGGGGGTACACAACAGCAACCTTGAGTATCTTGTGCTA 418
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 QY 431 ctccatgcccctccggaacctgtccctcggtgagaggtctccaggagaaagactcttg 490
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 Db 539 CAAACCTTAGAAGTCAATGATGTGTTCTTCAGCTCTCCATCTGCCCCGTCCAGGG 598
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 Db 599 TGTGCCCATGTGGGGGCAACGTGACCTGAGCTGCAGTCTCCAAGAGATGAAGCCCGC 658
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 QY 671 tgtccaataccagtggtgatcgagcttccatcctccagacttcttgcaccagcat 730
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 Db 659 TGTCAATACCAAGTGGGATCGGCAAGCTTCCATCTTCCAGACTTCTTTTGACACAGCAT 718
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 QY 731 agatgtcatccgtgggtcttgaagcctcaaccaacttctgtcttccatgctgaggtcta 790
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 Db 719 AGATGTATCCGTGGGTCTTTAAGCCTTCACCAACTTTCGTTCATGAGGTGAGTCTA 778
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 QY 791 tgtctgaagggccacatgaggtggtggtggtggtggtggtggtggtggtggtggtggtg 850
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 Db 779 TGTCTGCAAGGCCCAACATGAGGTGGGCACGTGCCAATGTATGTGACGCTGGAAGTGA 838
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| Query Match | 52.0%; | Score 942.6; | DB 9; | Length 1003; |
| Best Local Similarity | 99.6%; | Pred. No. 1.7e-212; | | |
| Matches 975; Conservative | 1; | Mismatches 0; | Indels 3; | Gaps |

| Qy | 793 | ctctgcaaggcccaatgagtggtggcactgccaatgtatgtgacgtgtaagtga | 852 |
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| Db | 780 | tttgcaagcccaatgatggtggcactgccaatgattatgacgctgagtgaca | 839 |

QY 853 caggcctcgagctcagtcggtctgtgagctgtgtggttacccctgttggactgggt 912
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 Db 840 CAGGGCTGAGACTGAGTGGTGTCTGAGACTGTGTGGTAACCTGTTGGACTGGGT 899
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 Db 900 TGCTGCTGGCTGTGT-CTCTGTATACACCGCCGGGCAAGGCCCTTGAGAGAG-CAGCCA 957
 QY 973 atgatacgaaggagatgc 991
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 Db 958 ATGATATCAAGAGATGC 976

RESULT 7
 AL571713/c
 LOCUS AL571713 955 bp mRNA linear EST
 16-FEB-2001
 DEFINITION AL571713 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1031Y109 3
 prime, mRNA sequence.
 AL571713
 ACCESSION AL571713
 VERSION AL571713.1 GI:12929283
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 955)
 Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source 1..955
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 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 207 a 247 c 300 g 200 t 1 others
 ORIGIN

Query Match 52.0%; Score 942; DB 9; Length 955;
 Best Local Similarity 99.7%; Pred. No. 2.3e-212;
 Matches 953; Conservative 1; Mismatches 1; Indels 1; Gaps

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 Db 955 AAGGCCACAAATGAGGT-GGCACTGCCAAATGTAATGTGACGCTGGAAGTAGCACAGG 897
 QY 858 cctgagctcagtggtgtgtcgtgagctgtgtggtacccctggttggacttgggtgtgt 917
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 Db 896 CTTGAGACTGCAGTGTTGCTTGAGAGCTGTGTGGTAACCTGTGACTGGGGTTGCTG 837
 QY 918 gctggctgtgtcctctgtaccacgcggggcaaggccctggagagccagccaatgat 977
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 Db 836 GCTGGCTGTGCTCTTGTATACACCGCCGGGCAAGGCCCTTGAGAGAGCCACCAATGAT 777
 QY 978 atcaagagatgcatgtctctcccgagccctgcccctggcccgaagatcagacaatc 1037
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 Db 776 ATCAAGAGAGATGCCATGTGCTCCCGGACCTGCGCCCAAGAGCTCAGACATATC 717
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 Db 716 TCCAAGATGGAGCCCTTCTCTGTATCTCCGACGAGCCCTCGGGCCACCCCATGGC 657
 QY 1098 cctccagcctgtgtcattgtaccaccccgagccagctctctccagccagcctgcctca 1157
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 Db 656 CTTCCAGGCTGTGTGATTAACCCGACGCGCAAGTCTTCAGCAGGCGCTGCCCTCA 597
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 Db 596 CCAAGACTGCCACGACAGATGGGGCCCACTTCAACCAATATCCCCCATCTGTGTGG 537
 QY 1218 gttctctctgtgtgtgagccgcatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1277
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 Db 536 GTTCTTCTCTGTGTGTGAGCGCATGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 477
 QY 1278 caagctgctctgtgtatgatgaccccaaccatcatgtgtcaaggaatttgggtctct 1337
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 Db 476 CAAGCTGCTCTCTGTATGATGACCCCACTCACTCATTTGGCTTAAGGATTTGGGTCT 417
 QY 1338 ccttctataagggtcaacctctagcacagaggcctgtgcatgtggaaagatcacactcc 1397
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 Db 416 CTTCTATAGGGGTCACTCTTAGCACAGAGCCTGATGATGGAAAGTCCACACTCC 357
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 Db 356 TGACCTTAGTACTGTGCCCACTCTTACTGTGGAAACCATCTCAGTAAGACC 297
 QY 1458 taagtgtccaggagacagaaggaaggaagtagtgatcttgaatttgggagagcctcca 1517
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 Db 296 TAAGTGTCCAGAGACAGAAGAGAAGAAAGTAGATCTGGAATTGGAGAGAGCTTCCA 237
 QY 1518 cccaccctgactcctcctatgaagccagctgtgaaatagtactcaccaagatga 1577
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 Db 236 CCCACCCTGACTCTCTTATGAAGCAGCTGTGAATTAAGTACTCACCACGAAGTGA 177
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 Db 176 GGGGAGAGACTTCCAGTCACTGAGTCTCCAGGCCCCCTTGATCTGTATACCCACCCCTA 117

Qy 1651 ttggtccaccctccagctccctgtatctgatataacctgtcaggtcgtgttaggtt 1710
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 Db 134 TTGGCTCCACTCCAGCTCCCTGTATTGATATAACCTGTGCAGGCTTGCTTAGGTTT 75
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 Qy 1711 tactg999caga99gaatcctctatcaaacatacatgaatatgtgtttc 1770
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 Db 74 TACTGGGGCAGAGGATGAGGATCTTATTATAAACAATGAATATGTGTTTTC 15
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 Qy 1771 atttgcgaatttaa 1784
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 Db 14 ATTGGCAATTAA 1
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 RESULT 9
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 LOCUS AL548482 16-FEB-2001
 DEFINITION AL548482 LTI_NFL006_PL2 Homo sapiens cDNA clone CSOD1014YD08 5
 prime, mRNA sequence.
 ACCESSION AL548482
 VERSION AL548482.1 GI:12883529
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 969)
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 source location/Qualifiers
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 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifestech.com URL :
 http://fulllength.invitrogen.com"
 BASE COUNT 177 a 289 c 293 g 208 t 2 others
 ORIGIN

Query Match 50.3%, Score 911.6; DB 9; Length 969;
 Best Local Similarity 98.6%; Pred. No. 3.7e-205;
 Matches 960; Conservative 2; Mismatches 7; Indels 5; Gaps

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 Db 1 GGGTGTGACGGCTCGGCTCCCGCGCAGCTCCGCGCTCGCGCMG-CTCGGCACCTGCA 59
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 72 ggtcgtgctcccgcgcgctggcgccccctgactccgtcccgccaggaggagggccatgatt 131
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 60 GGTCCGTGCGTCCCGCGGCTGGCGCCCTTGACTCCGTCCCGGCCAGGAGGCCATGATT 119
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 Qy 132 tccctcccggggccccctggtgacccaacttgctcggttcttctcctggggtgagtgc 191
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 Db 120 TCCTCCCGGGGCCCCCTGTGTACCAACTGTGCGGTTTGTCTTCCGTGGGCTGAGTGC 179
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 Qy 192 ctccgccccccctcgcgggccccagctgcaactgctattgccccgcaaccggctgcaggcg 251
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 Db 180 CTCGGCCCCCTCGCGGGGCCAGCTGCACCTGCTCCGCCCAACCGGTTGCAGCGC 239
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 Qy 252 gtgagggaggagggaagtgtgcttccagcgtgtacacctgacggggagggtgtcttca 311
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 Db 240 GTGAGGGAGGGGAAGTGTGCTTCCAGCGTGTACACTTGTGCACGGGAGGTGTCTTCA 299
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 Qy 432 tccatgccccccggaacctgtccctgcgctg99aggtctccag99aagactctggc 491
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 Db 420 TCCATGCCCTCCCGGAACCTGTCTCCCTCGGTGAGGGTCTCCAGGAAGACTCTGCG 479
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 Qy 492 ccctacagctgtctcgtgtaatgtgcaagacaagaaggaacttagggccacagcattc 551
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 Qy 552 aaaaccttagaactcaatgtactgttctcctccagctccctccatctcgtccagaggt 611
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 Qy 612 gtgccccatgtg99gggcaacgtgacccctgagctccaggtctccaagagtaagccgct 671
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QY 852 acaggcctggagctgcagctggtctgtctgagctgtgtgtggttacctgtgtgactggg 911
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QY 912 ttgtctgctggctgtgtctctctgttaccaccggggcaccctgagagcacc 971
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Db 899 TTGCTGGCTGGGCTGTCTCTTGTGA-CACCGCCGGGCAAGGCC--TGAGGAGCAACC 955
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Db 956 AATGATATHAAGGA 969
RESULT 10
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LOCUS AL549789 1109 bp mRNA linear EST
16-FEB-2001
DEFINITION AL549789 LTI_NFL006_PL2 Homo sapiens cDNA clone CSOD1054Y101 5
prime, mRNA sequence.
ACCESSION AL549789
VERSION AL549789.1 GI:12886119
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1109)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 204 a 337 c 327 g 238 t 3 others
ORIGIN

Query Match 50.2%; Score 911; DB 9; Length 1109;
Best Local Similarity 98.9%; Pred. No. 5.4e-205;
Matches 937; Conservative 1; Mismatches 6; Indels 3; Gaps

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Db 1 CTGGGTGTACGGGGCTGTGCTCCGCGCACGCTCCGGCCGTGCGCA-SCITGGCACTG 59
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Db 60 CAGGTCCGTGCGTCCCGCGGCTGGCGCCCTTAAGTCCGTCCCGGCCAGGAGGGCCATGA 119
QY 130 ttccctcccggggccccctggtgaccaaactgctcggttttcttccctgggctgagt 189
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Db 120 TTTCCTCCCGGGGCCCTGTGTACCACTTGCTGCGGTTTGTCTTGCGGCTGAGTG 179
QY 190 ccttcggccccctcgcgggccagctgcaactgcaacttgcccgccaaccggtgcag 249
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Db 180 CCCTGGGCCCCCTCGCGGGGCCAGCTGCACTGCACTTGCCGCCAACCGGTGCAAG 239
QY 250 cgttgagaggagggaagtgtgtctccagcgtgtgtacacttgcaaggaggagtgtct 309
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Db 240 CGGTGAGGAGGAGGGAAGTGTGCTTCAGCGTGTAACCTTGACAGGGGAGGTGCTT 299
QY 310 catccagccatgaggaggtgcccttctgtatgtgtcttcaacagaaagaaaggagg 369
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Db 300 CATCCAGCCATGGAGGTGCCCTTGTGATGTGTTCTTCAACAGAAAGAAAGAGAG 359
QY 370 atcagtggtgtcctacatcaatggtgtcacaaagcaaaactgtagtacctgtct 429
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Db 360 ATCAGGTGTGCTCTACATCAATGGGTACACAAGCAAACTGAGTATCTTGCTT 419
QY 430 actccatgcccctccggaacctgtccctcgcgctgagggtctccaggagaaagactctg 489
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Db 420 ACTCCATGCCCTCCCGGAACCTGTCTCGCGCTGGAGGCTCTCCAGAGAAAGACTCTG 479
QY 490 gccctcagctgtccgtgaatgtgcaagacaacaagcaaatctaggggccacagca 549
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Db 480 GCCCCTACAGCTGCTCGGTGATGTGCAAGACAAACAAGCAATATAGGGGCCACAGCA 539
QY 550 tcaaaaccttagaactcaatgtactgttccctccagctcctccatcctgcgctccea 609
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Db 540 TCAAACTTAGAAGTCAATGTACTGTCTCTCCAGCTCTCCATCTGCGCTCCAGG 599
QY 610 gtgtgccccatgtggyggaacgctgacccctgagctccagctcctcaaggagtaagccg 669
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QY 670 ctgtccaataaccagtggtgagtcggcagcttccatcctccagacttcttgcacagcat 729
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Db 660 CTGTCCAATACCAGTGGGATCGGACGCTTCCATCTTCCAGACTTTCTTGCACCAAGCAT 719
QY 730 tagatgtcatccgtggtgtcttaagctcacaacaccttcgtcttccatgctggaagtct 789
|||||
Db 720 TAGATGTATCCGTGGGTCTTAAAGCTCACCACCACTTTCGTTCCATGTGCTGAGTCT 779
QY 790 atgtctcgaagccacaaatgaggtgggcactgcccacatgtatgtacgctggaagtga 849
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Db 780 ATGTCTCAAGGCCCAATAGTAGTGGGACATGCCCAATGTATGTACGCTGGAAGTGA 839

OY 1698 cttgttagtcttctactggtggcagagatagggaatcctcttaataaactaatgaat 1757
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Db 80 CTTGGTTAGGTTTACTGGGGCAGAGATAGGGAATCTTTATTAACATAATGTAANT 21
OY 1758 atgtgtgttc 1768
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Db 20 ATTTGTGTAT 10

RESULT 14
AL546335 938 bp mRNA linear EST
LOCUS 16-FEB-2001
DEFINITION AL546335 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1031Y109 5
prime, mRNA sequence.

ACCESSION AL546335
VERSION AL546335.1 GI:12879351
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 938)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source 1..938
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1031Y109"
/clone_lib="LTI_NFL006_PL2"
/issue_type="placenta"
/note="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dt) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the PCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 168 a 282 c 281 g 205 t 2 others
ORIGIN

Query Match 49.4%; Score 895.8; DB 9; Length 938;
Best Local Similarity 99.0%; Pred. No. 2e-201;
Matches 930; Conservative 2; Mismatches 4; Indels 3; Gaps

OY 10 ctgggtcagcgctcgcgtcccgagcagctcggcgctcgcgagcagctcgacactg 69
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Db 1 CTGGGTCACGGGCTTCGGCTCCGGCAGCAGCTCCGGCCGTCGCGCA-SCTCGGACCTG 59
OY 70 caggtccgtgcgtcccgcgctggcgccctgactccgtcccgccaggagggccatga 129
|||||
Db 60 CAGGTCCGTGCTCCGGCGGCTGCGCCCTGACTCCGTCCCGGCCAGGAGGGCCATGA 119
OY 130 ttccctcccgggccctggctgaccaactgctgcggttttcttccctggggtgagt 189
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Db 120 TTTCCCTCCCGGGGCCCTGTGACCAACTTGCTGGGTTTGTCTCTGGGGCTGAGTG 179

OY 190 ccctgcgccccctcgcgggccagctgcaactgcaactgcccgaacgggtgcagg 249
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Db 180 CCTCGCGCCCCCTCGCGGGGCCAGCTGCACTGACCTTGCCGCCAACCGGTTGCAGG 239

OY 250 cggtagagggaggagtggtgtctccagcgtgtaacacttgcaaggagggtgtct 309
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Db 240 CGGTGAGAGGAGGAGGAGTGTGCTTCCAGCGTGTACACCTTGACAGGGGAGTGTCTT 299

OY 310 catcccaagcattgggagtgcccttgatgtgttctcaacagaaagaaaggagg 369
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Db 300 CATCCAGCCATGGAGAGTGCCCTTGTGTGTCTTCAACAGAAAGAAAGAGG 359

OY 370 atcagtggtgtcctacatcaatgggggtcacaaagcaaacctggagatcctgtgtc 429
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Db 360 ATCAGGTGTGTCTACATCAATGAGGTCACAAACCAACTGAGTATCTTGCTGTCT 419

OY 430 actccatgcccctcccggaacctgtccctcggtgtaggggtctccaggagaagactctg 489
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Db 420 ACTCCATGCCCCCTCCGGAACCTGTCTCCCTGCGGCTGAGGGTCTCCAGAGAAAGACTCTG 479

OY 490 gccctcaagctgtccgtgaatgtgcaagacaagaagcaaatctaggggccacagca 549
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Db 480 GCCCCTACAGCTGCTCGTGAATGTGCAAGACAAGCAAACTTAAGGGGCACAGCA 539

OY 550 tcaaaccttagaactcaatgactgtgtccctccagctccctccatccgtccgtctccagg 609
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Db 540 TCAAAACCTTAGAACTCAATGACTGTCTCCCTCCAGCTCCATCTCGCCGTCTCCAGG 599

OY 610 gtgtgccccatgtgggggcaaacgtgacccctgagctccagctctccaaggagtaagcccg 669
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Db 600 GTGTGCCCATGTGGGGCAACGTCGCTGAGCTGCCAGTCTCCAGGAGTAAGCCCG 659

OY 670 ctgtccaataccagtggtgagtcggcagcttccatccctccagacttcttgcaccagcat 729
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Db 660 CTGTCCAATACAGTAGGAGTCGGCAGCTTCCATCTTCCAGACTTCTTGGACACAGCAT 719

OY 730 tagatgtcatccgtggtgtcttaagctcaccacaacttgcgtcttccatgctgaggtct 789
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Db 720 TAGATGTATCCTGCTGGGTCTTAAGCCTCACCAACTTTGCTTCCATGGCTGGAGTCT 779

OY 790 atgtctgcaagggccacaatgaggtgggcaactgcccaatgtaatgtacgctggaagtga 849
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Db 780 ATGTCTGCAAGGCCACCAATGAGGTGGGACACTGCCCAATGTATGTGACGCTGGAAGTGA 839

OY 850 gcaacagggcctggagctgcagtggtgtctggagctgtgtgggtaccctggttgactgg 909
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Db 840 GCACAGGGCCTGAGAGCTGCAATGTGCTGTGAGCTGTGTGGGTA-CCTGTGGACTGG 898

QY 910 ggttgctgctggcgtgctcctctgtaccacgcccggg 948
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Db 899 GGTGTGCTGGCTGGCTGGT-CTTTGTATCAACGCGGGG 936

RESULT 15
AL554790 999 bp mRNA linear EST

16-FEB-2001
DEFINITION AL554790 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI086YJ14 5
prime, mRNA sequence.

ACCESSION AL554790
VERSION AL554790.1 GI:12895912
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 999)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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location/Qualifiers
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/db_xref="taxon:9606"
/clone="CSODI086YJ14"
/clone_lib="LTI_NFL006_PL2"
/issue_type="piacenta"
/note="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the PCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 184 a 298 c 302 g 214 t 1 others
ORIGIN
Query Match 49.4%; Score 895.8; DB 9; Length 999;
Best Local Similarity 98.8%; Pred. No. 2.1e-201;
Matches 934; Conservative 0; Mismatches 7; Indels 4; Gaps 3;

QY 12 ggggtgcagcggcgtcggtcccgcgacgctccggcgtcgcgacgctcgacactgca 71
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Db 1 GGGTGTACGGCGCTCGGCTCCCGCGACGCTCCGGCGCTCGCGCA-CTTCGGCACCCTGCA 59

QY 72 ggtccgctgctcccgcggtcgcgccccctgaactcgctcccgcgccaggaggacatgatt 131
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Db 60 GGTCCGTGCTGCCCGCGGCTGGCGCCCTTGACTCCGTCCCGGCCAGGAGGAGCCATGATT 119

QY 132 tccctcccggggcccctggtgacccaactgtctcgsgtlttgttccctggggctgaatgac 191
|||||
Db 120 TCCCTCCCGGGGCCCTGTGTACCAACTTGTCTGGGTTTTTTTCTCTGGGGCTGAGTGCC 179

QY 192 ctgcgccccctcgcggcccaactgcaactgtcccgcccaaccggtgtcgagcg 251
|||||
Db 180 CTGCGGCCCCCTCGGGGGCCAGCTGCAACTGTGACCTTGCCGCCCAACCGGTGACAGCG 239

QY 252 gtggaaggagggaatggtgtgtctccaagcgtgtgtacaactgtgacggggaggtgtctca 311
|||||
Db 240 GTGAGGGAGGGGAAGTGTGTCTTCCAGCTGTGTACACTTGTGACGCGGGAGGTGTCTTCA 299

QY 312 tcccaagccatggagggtgccccttgtgatgtgttcttcaacagagaagaaggagat 371
|||||
Db 300 TCCAGCCATGGAGGTGCCCCCTTGTGTATGTGTCTTCAACAGAAAGAAAGAGAGAT 359

QY 372 caggtgtgtctctacatcaatggtgggtcacacaagaacaacctggagratcctgtgtctac 431
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Db 360 CAGGTGTGTCTCTACATCAATGGGGTCAACAAGCAAACTGGAGTATCTTGTGTCTAC 419

QY 432 tccatgcccctccggaacctgtccctcgctggaagggtctccagsgaagaactctggc 491
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Db 420 TCCATGCCCTCCCGGAACCTGTCTCCCTGCGGTGAGGGTCTCCAGGAAAGACTCTGGC 479

QY 492 ccctacagctgtccgtgatgtgcaagacaagaaggaacttaagggtccacagcatc 551
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Db 480 CCTACAGCTGTCTCCGATGTGCAAGACAAACAAGCAAACTAGGGGCCACAGCATC 539

QY 552 aaaaccttagaactcaatgtactgttccctccagctcctccatcctcgcttccagggt 611
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Db 540 AAAACCTTAGAACTCAATGTACTGTCTCTCCAGCTCTCCATCTGCGGTCTCCAGGGT 599

QY 612 gtcgcccatgtgggggcaaacgtgacacctgagctgacgtctccaaggagtaagccgct 671
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Db 600 GTGCCCATGTGGGGGCAACGTGACCTGACCTGACGTCTCCAAAGAGTAAGCCGCT 659

QY 672 gtccaatcacagtggtggtcgcgacgttccatccttccagacttctttgacacagcatla 731
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Db 660 GTCCAATCACAGTGGGATCGGACGCTTCCATCTTCCAGACTTTCTTTGACACAGCATTA 719

QY 732 gatgtcatcgtgggtctttaaagcctcaacacaccttcgtcttccatggtcgtgagtcctat 791
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Db 720 GATGTCACTCCGTGGGTCTTTAAGCTCAACCACTTTCGCTTCCATGAGCTGAGTCTAT 779

QY 792 gttcgaagggcccaatgaggtgggacctgcccacgttaatgtgacgtcgtgaagtgaac 851
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Db 780 GTCTGCAAGGCCCAACATGAGGTGGGACATGCAAAATGTAATGTGACGCTGAAAGTAGC 839

QY 852 acaaggcctgtagctgtagtgtgtctcgtgagctgtgtgtggttaacctggttggactgggg 911
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Db 840 ACAGGGCCTGAGCTGAGTGTGTCTTGTGAGCTGTGTGTGGTA-CTTGCTTGAAGTGGGG 898

QY 912 ttgtcgtgctgggctgtgtcctctgtacacacccgggggcaaggcc 956
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Db 899 TTGCTGCTGGGCTGTGTC--TCTTGTACACCGCGGGGCAAGGCC 941

Search completed: August 19, 2002, 15:31:47
Job time: 1850 sec

ALIGNMENTS

RESULT 1

CXAR_MOUSE

ID CXAR_MOUSE STANDARD; PRT; 365 AA.
AC P97792; O09052;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cocksackievirus and adenovirus receptor homolog precursor (mCAR).
GN CXADR OR CAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Cocksackie B viruses and
RT adenoviruses 2 and 5.";
RL Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/MAI;
RX MEDLINE=97250541; PubMed=9096397;
RA Tomko R.P., Xu R., Philipson L.;
RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B coxsackieviruses.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Bergelson J.M., Krithivas A., Crowell T.L., Finberg R.W.;
RT "The murine CAR homologue (mCAR) is a receptor for coxsackie B
RT viruses and adenoviruses.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; Y10320; CAA71368.1; -.
DR EMBL; U90715; AAC53148.1; -.
DR EMBL; Y11929; CAA72679.1; -.
DR MGD; MGI:1201679; Cxadr.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00410; IG_like; 1.

DR SMART; SM00408; IGc2; 1.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
 FT HOMOLOG.
 FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 41 120 BY SIMILARITY.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 340 365 VAAPNLSRMGAVPVMIPAQSKDGSIV -> FKYAYKTDGIT
 FT VV (IN REF. 2 AND 3).
 SQ SEQUENCE 365 AA; 39947 MW; 5445B4B52A34B2A2 CRC64;

Query Match 17.6%; Score 353.5; DB 1; Length 365;
 Best Local Similarity 27.8%; Pred. No. 1.8e-16;
 Matches 113; Conservative 71; Mismatches 156; Indels 67; Gaps 15;

Qy 9 VTNLLRFLFL-GLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSSQPWE 67
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 Db 1 MARLLCFVLLCGIADFT----SGLSITTPEQRIEKAKGETAYLPCKFTLSPE--DQGPLD 54
 Qy 68 VPFVWMWFFKQKEKE--DQVLSYINGVTTSKPGVSLVY-----SMPSRNL 109
 : : | : : ||| : : | : | : : : | : :
 Db 55 IE---WLISPSDNQIVDQVIILYSG-----DKIYDNYYPDLKGRVHFTSNDVKSGDA 103
 Qy 110 SLRLEGLQEKGDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGAN 169
 | : : || | | | | | : | : | | | | | : | :
 Db 104 SINVTNLQLSDIGTYQCKVK-----KAPGVANKKFLTLVLVKPSGTRCFVDGSEEIGND 157
 Qy 170 VTLSCQSPRSKPAVQYQWDRQLPSFQTFAPAL-DVIRGSLSLTNLSSSMAGVYVCKAHN 228
 | | : : : : | : | | : : : : | | : | | |
 Db 158 FKLKCEPKESLPLQFEW-QKLSDSQTMTPTWLAEMTSPVISVKNASSEYSGTYSCTVQN 216
 Qy 229 EVGTAQCNTLE-VSTGPGAADVAGAVVGTLLVGLGLLAGLVLLYHRR---GKALEEPAND 284
 || : || : | : | : |||| : || : | : : || : | :
 Db 217 RVGSDQCMLRLDVPPSNRAGTIAGAVIGTLLALVLIGAILFCCHRRKREEKYEKEVHHD 276
 Qy 285 IKEDAIAPRTLPPWKSSDTISKNGTLSSSVTSARALRPPHGP RP GALTPTPSLSSQALPS 344
 | : || : | ||| : : : | : : | : : : | :
 Db 277 IRED-----VPPPKSRTSTARSYIGSNHSSL-----GSMSPSNMEGYSKTQY 318
 Qy 345 PRLPTTDGAH-PQPISSIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
 : : | : | : | : | : ||||| : |||| : || :
 Db 319 NQVPSEDFERAPQSPTLAPAKVAAPNLSRMGAVPVMIPAQSKDGSIV 365

RESULT 2

CXAR_HUMAN

ID CXAR_HUMAN STANDARD; PRT; 365 AA.
AC P78310; O00694;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cocksackievirus and adenovirus receptor precursor (Cocksackievirus B-
DE adenovirus receptor) (hCAR) (CVB3 binding protein).
GN CXADR OR CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Cocksackie B viruses and
RT adenoviruses 2 and 5.";
RL Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97250541; PubMed=9096397;
RA Tomko R.P., Xu R., Philipson L.;
RT "hCAR and mCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B coxsackieviruses.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20008750; PubMed=10543405;
RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
RA Bowles N.E.;
RT "Genomic organization and chromosomal localization of the human
RT Cocksackievirus B-adenovirus receptor gene.";
RL Hum. Genet. 105:354-359(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;
RT "Sequence and expression of CXADR, the human gene for the
RT coxsackievirus and adenovirus receptor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y07593; CAA68868.1; -.
DR EMBL; U90716; AAC51234.1; -.
DR EMBL; AF169366; AAF05908.1; -.
DR EMBL; AF169360; AAF05908.1; JOINED.

Query Match 17.0%; Score 343; DB 1; Length 365;
Best Local Similarity 27.5%; Pred. No. 9e-16;
Matches 106; Conservative 67; Mismatches 147; Indels 66; Gaps 14;

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| Qy | 31 | LQLHLHPANRLQAVEGGEVVLPAWYTLHGEVSSSQPWVEVPFVMWFFK--QKEKEDQVLSYI | 88 |
| | | : : : : : : : : | |
| Db | 20 | LSITTPEEMIEKAKGETAYLPCKFTLSPE--DQGPLDIE---WLISPADNQKVDQVIILY | 74 |
| Qy | 89 | NGVTTSKPGVSLVY-----SMPSRNLSLRLEGLQEKDSGPYSCSVNVQD | 132 |
| | | : : : : : : : : : | |
| Db | 75 | SG-----DKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVK--- | 123 |
| Qy | 133 | KQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSKPAVQYQWDRQLP | 192 |
| | | : : : : : : : : : : : | |
| Db | 124 | ---KAPGVANKKIHLVVLVKPSGARCYYVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSD | 180 |
| Qy | 193 | SFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE-VSTGPGAAVVA | 251 |
| | | : : : : : : : : : : | |
| Db | 181 | SQKMPTSWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSDQCLLRNLNVPPSPNKAGLIA | 240 |
| Qy | 252 | GAVVGTLVGLGLLAGLVLLYHRRGKALE---EPANDIKEDAIAPRTLWPWKSSDTISK | 307 |
| | | : : : : : : : : : : : : | |
| Db | 241 | GAIIGTLLALALI-GLIIFCCRKKRREEKYEKEVHHDIRE-----VPPPKSRTSTARS | 293 |
| Qy | 308 | GTLSSVTSARALRPPH--GPPRPGALTPTPSLSSQALP-SPRLPTTDGAHPQPISPIPGG | 364 |
| | | : : : : : : : : : | |
| Db | 294 | YIGSNHSSLGSMSPSNMEGYSKT-QYNQVPSEDFERTPQSPTLP-----PAK | 339 |
| Qy | 365 | VSSSGLSRMGAVPVMVPAQSQAGSLV | 390 |
| | | : : : : : : | |
| Db | 340 | VAAPNLSRMGAIPVMIPAOSKDGSIIV | 365 |